

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:13:59 ; Search time 1420 Seconds  
(without alignments)  
32.939 Million cell updates/sec

Title: US-10-006-190-1  
Perfect score: 1161  
Sequence: 1 MGASARLRRAVIMGAPGSGK.....VYAFIQTKVPQRSQKASYTP 227

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*

- 1: sp-archaea:\*
- 2: sp-bacteria:\*
- 3: sp-fungi:\*
- 4: sp-human:\*
- 5: sp-invertebrate:\*
- 6: sp-mammal:\*
- 7: sp-mhc:\*
- 8: sp-organelle:\*
- 9: sp-phage:\*
- 10: sp-plant:\*
- 11: sp-rodent:\*
- 12: sp-virus:\*
- 13: sp-vertebrate:\*
- 14: sp-unclassified:\*
- 15: sp-virus:\*
- 16: sp-bacteriap:\*
- 17: sp-archaeap:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1156	99.6	227	4 Q9NPB4	Q9NPB4 h cDNA flj1
2	1078	92.9	227	4 Q9D721	Q9D721 mus musculu
3	1074	92.5	227	11 Q9DBM5	Q9DBM5 mus musculu
4	1073	92.4	227	11 Q9DBM5	Q9DBM5 mus musculu
5	1054	90.8	227	6 Q9S394	Q9S394 oryctolagus
6	899	77.4	189	11 Q9D8W6	Q9D8W6 mus musculu
7	809	69.7	157	4 Q9HC01	Q9HC01 homo sapien
8	698	60.1	136	4 Q9H576	Q9H576 homo sapien
9	565	48.7	216	5 Q9VG06	Q9VG06 drosophila
10	439	37.8	248	10 Q9FK35	Q9FK35 arabidopsis
11	438	37.7	221	16 Q8R7X4	Q8R7X4 thermozear
12	433.5	37.3	231	3 Q9S985	Q9S985 neocallimias
13	424	36.5	231	3 Q9S987	Q9S987 piromyces s
14	413	35.6	232	11 Q9CY37	Q9CY37 mus musculu
15	411	35.4	232	3 Q93986	Q93986 neocallimias
16	399	34.4	209	10 Q9MAY0	Q9MAY0 oryza sativ

17	398.5	34.3	240	5 Q9U915	Q9U915 drosophila
18	393	33.9	220	5 Q9Y0A8	Q9Y0A8 cryptospori
19	385.5	33.2	215	17 Q8TR53	Q8TR53 methanosarc
20	378	32.6	237	5 Q9W1D0	Q9W1D0 drosophila
21	365	31.4	202	4 Q8TCY3	Q8TCY3 homo sapien
22	364.5	31.4	159	2 Q9G011	Q9G011 haemophilus
23	364	31.4	159	2 Q9G0D4	Q9G0D4 haemophilus
24	364	31.4	159	2 Q9G0C4	Q9G0C4 haemophilus
25	364	31.4	159	2 Q9G012	Q9G012 haemophilus
26	364	31.4	159	2 Q9AM09	Q9AM09 haemophilus
27	362.5	31.2	220	17 Q8U207	Q8U207 pyrococcus
28	360	31.0	159	2 Q9G0C7	Q9G0C7 haemophilus
29	358.5	30.9	211	16 Q8RE31	Q8RE31 fusobacteri
30	329.5	28.4	588	10 Q8VYX1	Q8VYX1 arabidopsis
31	323	27.8	155	2 Q9R452	Q9R452 neisseria m
32	323	27.8	155	2 Q9R452	Q9R452 neisseria m
33	322	27.7	155	2 Q9R452	Q9R452 neisseria m
34	321	27.6	216	1 Q9P9D2	Q9P9D2 uncultured
35	319.5	27.5	217	10 Q9FY07	Q9FY07 arabidopsis
36	319	27.5	283	10 Q9F1D7	Q9F1D7 arabidopsis
37	315	27.1	155	2 Q9R452	Q9R452 neisseria m
38	305	26.3	149	3 Q96VQ1	Q96VQ1 neocallimias
39	303	26.1	149	3 Q96VQ2	Q96VQ2 piromyces s
40	294.5	25.4	151	3 Q96VQ0	Q96VQ0 neocallimias
41	292.5	25.2	269	5 Q9N910	Q9N910 leishmania
42	280	24.1	229	5 Q9Y0E7	Q9Y0E7 leishmania
43	278.5	24.0	196	16 Q8UE38	Q8UE38 agrobacteri
44	271	23.3	284	10 Q9ZU01	Q9ZU01 arabidopsis
45	268	23.1	130	4 Q8TCY2	Q8TCY2 homo sapien

#### ALIGNMENTS

##### RESULT 1

Q9NPB4 PRELIMINARY: PRT: 227 AA.

AC Q9NPB4: 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)  
 DE CDNA FLJ11089 fis, clone PLACE1005305, highly similar to GTP:AMP  
 DE phosphotransferase mitochondrial (EC 2.7.4.10) (CDNA FLJ10691 fis,  
 DE clone NT2RP3000359, highly similar to GTP:AMP phosphotransferase  
 DE mitochondrial) (CDNA FLJ14628 fis, clone NT2RP2000329, highly similar  
 DE to GTP:AMP phosphotransferase mitochondrial) (Hypothetical 25.6 kDa  
 DE protein).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,  
 RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,  
 RA Nakamura Y., Nagahari K., Masuno Y., Sasaki N.,  
 RA "NEO human cDNA sequencing project."  
 RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,  
 RA Tanai H., Kimata M., Watanabe M., Hirooka S., Ishii S., Kawai Y.,  
 RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,  
 RA Masuno Y., Kanehori K.,  
 RA "NEO human cDNA sequencing project."  
 RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

RA Wagatsuma M., Hosoliri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takenashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,  
 RA Niimiya K., Iwayanagi T.,  
 RT "NEO human cDNA sequencing project."  
 RN Submitted (May-2001) to the EMBL/Genbank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-LYMPH:  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 DR EMBL; AK001951; BAA91996.1; -;  
 DR EMBL; AK001553; BAA91753.1; -;  
 DR EMBL; AK027534; BAB55183.1; -;  
 DR EMBL; BC013771; AAH13771.1; -;  
 DR HSSP; P08760; 2AK3.  
 DR InterPro; IPR000850; Adenylate\_kin.  
 DR InterPro; IPR000623; Shk\_kinase.  
 DR Pfam; PF00406; adenylatekinase; 1.  
 DR PRINTS; PR00094; ADENYLTKINASE.  
 DR PRINTS; PR01100; SHIKIMTKINASE.  
 DR Prodom; PD000657; Adenylate\_kin; 1.  
 DR PROSITE; PS00113; ADENYLATE\_KINASE; 1.  
 KW Hypothetical protein; kinase; transferase.  
 SQ SEQUENCE 227 AA; 25565 MW; 98A0EDFAFD9C9CF64;

Query Match 99.6%; Score 1156; DB 4; Length 227;  
 Best Local Similarity 99.1%; Pred. No. 3,1e-94;  
 Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MGASARLLRAVIMGAPGSGKGVSSRITTFELKHLSSGDLRDNMRLRGTETGLAKAFI 60  
 DB 1 MGASARLLRAVIMGAPGSGKGVSSRITTFELKHLSSGDLRDNMRLRGTETGLAKAFI 60  
 OY 61 DOGKLIIPDDVMTRLALHELKNTLTQCSWLDGFPRTLPOAEALDRAYQIDVTINLVNPFV 120  
 DB 61 DOGKLIIPDDVMTRLALHELKNTLTQCSWLDGFPRTLPOAEALDRAYQIDVTINLVNPFV 120  
 OY 121 IKORLTARWIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDDBPEYIKRLKAYEQT 180  
 DB 121 IKORLTARWIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDDBPEYIKRLKAYEQT 180  
 OY 181 KXVLXYOKKGVLETFSGTETNKIMPYVYAFLOTQVPPQSRQASVTP 227  
 DB 181 KPVLEYOKKGVLETFSGTETNKIMPYVYAFLOTQVPPQSRQASVTP 227

RESULT 2

99D721 PRELIMINARY: PRT: 227 AA.

ID 09D721  
 AC 09D721  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Adenylate kinase 3 alpha like.  
 GN AKJ3L.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID-10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6J; TISSUE-STOMACH;  
 RX MEDLINE-21085660; PubMed-11217851.  
 RA Kawai J., Shunagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiya H.,  
 RA Kuehl P., Lewis S., Matsuno Y., Nakai I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staab F., Suzuki R., Tomita M., Wagner L., Mashio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guslinich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schenbach C., Seta T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-COLON;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.

RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 DR EMBL; BC016432; AAH16432.1; -;  
 DR EMBL; BC019174; AAH19174.1; -;  
 DR EMBL; BC024871; AAH24871.1; -;  
 DR HSSP; P08760; 2AK3.  
 DR MGD; MGI:1860835; AKJ3L.  
 DR InterPro; IPR000850; Adenylate\_kin.  
 DR InterPro; IPR000623; Shk\_kinase.  
 DR Pfam; PF00406; adenylatekinase; 1.  
 DR PRINTS; PR00094; ADENYLTKINASE.  
 DR PRINTS; PR01100; SHIKIMTKINASE.  
 DR Prodom; PD000657; Adenylate\_kin; 1.  
 DR PROSITE; PS00113; ADENYLATE\_KINASE; 1.  
 KW kinase; transferase.  
 SQ SEQUENCE 227 AA; 25426 MW; 6601D10971DE5AC CRC64;

Query Match 92.9%; Score 1078; DB 11; Length 227;  
 Best Local Similarity 92.1%; Pred. No. 2,4e-87;  
 Matches 209; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

OY 1 MGASARLLRAVIMGAPGSGKGVSSRITTFELKHLSSGDLRDNMRLRGTETGLAKAFI 60  
 DB 1 MGASARLLRAVIMGAPGSGKGVSSRITTFELKHLSSGDLRDNMRLRGTETGLAKAFI 60  
 OY 61 DOGKLIIPDDVMTRLALHELKNTLTQCSWLDGFPRTLPOAEALDRAYQIDVTINLVNPFV 120  
 DB 61 DOGKLIIPDDVMTRLALHELKNTLTQCSWLDGFPRTLPOAEALDRAYQIDVTINLVNPFV 120  
 OY 121 IKORLTARWIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDDBPEYIKRLKAYEQT 180  
 DB 121 IKORLTARWIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDDBPEYIKRLKAYEQT 180  
 OY 181 KXVLXYOKKGVLETFSGTETNKIMPYVYAFLOTQVPPQSRQASVTP 227  
 DB 181 EPNLYOKKGVLETFSGTETNKIMPHYVYAFLOTQVPPQSRQASVTP 227

RESULT 3

99DBM5 PRELIMINARY: PRT: 227 AA.

ID 99DBM5  
 AC 99DBM5  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Adenylate kinase 3 alpha like.  
 GN AKJ3L.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=LIVER;  
RX MEDLINE=21085660; Pubmed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
Rieschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,  
Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,  
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilmink L.,  
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
Hayashizaki Y.;  
RA "Functional annotation of a full-length mouse cDNA collection.";  
RT Nature 409:685-690(2001).  
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
DR EMBL: AK004864; BAB23625.1; -;  
DR HSSP: P08760; 2AK3.  
DR MGD: MGI:1860835; AK131.  
DR InterPro: IPR000850; Adenylate\_kin.  
DR InterPro: IPR000623; Shik\_kinase.  
DR Pfam: PF00406; adenylatekinase; 1.  
DR PRINTS: PR00094; ADENYLTKINASE.  
DR PRINTS: PR01100; SHIKIMTKINASE.  
DR PRODOM: PD000657; Adenylate\_kin; 1.  
DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
KW kinase; transferase.  
SQ SEQUENCE 227 AA; 25427 MW; 680FDF1E91DE5AC CRC64;  
  
Query Match 92.5%; Score 1074; DB 11; Length 227;  
Best Local Similarity 91.6%; Pred. No. 5.4e-87;  
Matches 208; Conservative 8; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 MGASARLLRAVINGAPSGKGTSSRTTTFELKHLSSGDLRLDNLGTEIGYLAKAFI 60  
DB 1 MGASGRLLRAVINGAPSGKGTSSRTTKHPELKHLSGDLRLQNMLOGTEIGYLAKTFI 60  
  
QY 61 DQGLIPDDVWTRIALHELNLTQYSWLDGFPRTLPQAEALDRAVYIDIVININVPFV 120  
DB 61 DQGLIPDDVWTRIALHELNLTQCSWLDGFPRTLPQAEALDRAVYIDIVININVPFV 120  
  
QY 121 IKORLTARWHPASGRVYNIEFNPPTKVGIDDLGEPFLIOREDKPEPTVIRLKA YEQT 180  
DB 121 IKORLTARWHPASGRVYNIEFNPPTKVGIDDLGEPFLIOREDKPEPTVIRLKA YEQT 180  
  
QY 181 KXVLXYQKKGVLTFESGTEFNKIMPVYAFLOTKVPQORSOKASVTP 227  
DB 181 EPVLQYQKKGVLTFESGTEFNKIMPVYAFLOTKVPQORSOKASVTP 227  
  
RESULT 4  
Q9DB57 PRELIMINARY; PRT; 227 AA.  
ID Q9DB57;  
AC Q9DB57;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Adenylate kinase 3 alpha like.  
GN AKL3L.  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;  
RX MEDLINE=21085660; Pubmed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
Rieschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,  
Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,  
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilmink L.,  
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
Hayashizaki Y.;  
RA "Functional annotation of a full-length mouse cDNA collection.";  
RT Nature 409:685-690(2001).  
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
DR EMBL: AK005194; BAB23876.1; -;  
DR HSSP: P08760; 2AK3.  
DR MGD: MGI:1860835; AK131.  
DR InterPro: IPR000850; Adenylate\_kin.  
DR InterPro: IPR000623; Shik\_kinase.  
DR Pfam: PF00406; adenylatekinase; 1.  
DR PRINTS: PR00094; ADENYLTKINASE.  
DR PRINTS: PR01100; SHIKIMTKINASE.  
DR PRODOM: PD000657; Adenylate\_kin; 1.  
DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
KW kinase; transferase.  
SQ SEQUENCE 227 AA; 25427 MW; 660B7FBA971DE5AC CRC64;  
  
Query Match 92.4%; Score 1073; DB 11; Length 227;  
Best Local Similarity 91.6%; Pred. No. 6.6e-87;  
Matches 208; Conservative 8; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 MGASARLLRAVINGAPSGKGTSSRTTTFELKHLSSGDLRLDNLGTEIGYLAKAFI 60  
DB 1 MGASGRLLRAVINGAPSGKGTSSRTTKHPELKHLSGDLRLQNMLOGTEIGYLAKTFI 60  
  
QY 61 DQGLIPDDVWTRIALHELNLTQYSWLDGFPRTLPQAEALDRAVYIDIVININVPFV 120  
DB 61 DQGLIPDDVWTRIALHELNLTQCSWLDGFPRTLPQAEALDRAVYIDIVININVPFV 120  
  
QY 121 IKORLTARWHPASGRVYNIEFNPPTKVGIDDLGEPFLIOREDKPEPTVIRLKA YEQT 180  
DB 121 IKORLTARWHPASGRVYNIEFNPPTKVGIDDLGEPFLIOREDKPEPTVIRLKA YEQT 180  
  
QY 181 KXVLXYQKKGVLTFESGTEFNKIMPVYAFLOTKVPQORSOKASVTP 227  
DB 181 EPVLQYQKKGVLTFESGTEFNKIMPVYAFLOTKVPQORSOKASVTP 227  
  
RESULT 5  
Q95J94 PRELIMINARY; PRT; 227 AA.  
ID Q95J94;  
AC Q95J94;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Adenylate kinase 3.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.











Dt	01-MAR-2002 (TreeBlastrel_20, last annotation update)
Dr	Adenylylate kinase (EC 2.7.4.3) (Fragment).
Gn	HDCAK12.2.
Oc	Neocallimastix frontalis (Rumen fungus).
Oc	Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
Ox	Neocallimasticaceae; Neocallimastix.
Rn	NCBI_TaxID=4757;
Rp	[1]
Rc	SEQUENCE FROM N.A.
Ra	STRAIN=L2;
Ra	Voncken F., Boxma B., Verhagen E., van Wesel R., van der Drift C.,
Ra	Veenhuis M., Hackstein J., Vogels G.;
Rl	"Evidence for a chimeric origin of chytrid hydnosomes."
Rl	Submitted (FEB-1998) to the EMBL/Genbank/DDP databases.
Cc	-I-SIMILARITY: BELONGS TO THE ADENYLYATE KINASE FAMILY.
Dr	EMBL: AJ224659; CAAL2056.1; "
Dr	HSSP; P07170.1AKY.
Dr	InterPro: IPR000850; Adenylylate_kin.
Dr	Pfam: PF00406; adenylylatekinase. 1.
Dr	PRINTS; PR00094; ADENYLTKINASE.
Dr	Prodrom: PD000657; Adenylyate_kin. 1.
Kw	PROSITE: PS00113; ADENYLYATE_KINASE; 1.
Ft	kinase; transferase.
Ft	NON_TER 232
So	SEQUENCE 232 AA; 25441 MW; 1B74EFD7C97891F2 CRC64;
Query Match	35.4%; Score 411; DB 3; Length 232;
Best Local Similarity	41.4%; Pred. No. 2,le-28;
Matches	94; Conservative 38; Mismatches 73; Indels 22; Gaps
Oy	4 SALLRLAVINGAPSGGKGTVSSRTITHELKLHSSGDLDRDNLMTGLTGLAKAFIDOG 63
Db	6 SKNSLRVMVPPGGCKSTOAPKVYCDYCICHLADGLRAVLKAGTPIGMEAKKIMDAG 65
Oy	64 KLIPDDVMTRLAHLE-----KNLTQYSMLDGPEPTLLPOAALD----RAYQIDVTYN 113
Db	66 GLVSEIIVNLIKELMDTRACKN---GITLDGFPRYAQAOKLDEMLEQRNKOLDTAE 121
Oy	114 LNVPEVIKQRLTAARIHPASGRVYNIIEFN-PKTVGIDIDLGEPLIOREDKPETVIKR 172
Db	122 LTVDLSLFLFKRTTGTLVHPASGRSYHKLFENPNQKEGKDIDIGEPLIQSDSTEALKKR 181
Oy	173 LKAVEDDKXYLVXYYOKKGVLTEFSGETENK----TWPYVAFLDTQ 215
Db	182 LVATHKQTVPVADYIKKKGI--MGVVASOPPAAVWMAQMOMAFISEK 225

Search completed: March 19, 2003, 16:32:44  
Job time : 1423 secs

GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 15:24:06 ; Search time 690 seconds  
(without alignments)  
31.627 Million cell updates/sec

Title: US-10-006-190-1

Perfect score: 1161

Sequence: 1 MGASARLLRAVIMGAPGSGK.....VYAFLOTQVPOBSQKASVTP 227

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR-73:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1091	89.4	227	2 A34442	nucleoside-triphos
2	1038	89.4	227	2 JQ1945	nucleoside-triphos
3	700.5	60.3	223	1 K1H0A3	adenylate kinase
4	447.5	38.5	214	2 I64062	adenylate kinase
5	439.5	37.9	225	2 S23568	adenylate kinase
6	437	37.6	217	2 T44404	adenylate kinase
7	436	37.6	220	2 S31338	adenylate kinase
8	435	37.5	222	1 K1BYA	adenylate kinase
9	431	37.1	222	2 JC5893	adenylate kinase
10	431	37.1	229	2 G02248	adenylate kinase
11	430	37.0	215	2 S61841	adenylate kinase
12	430	37.0	215	2 F81154	adenylate kinase
13	428	36.9	218	2 S43016	adenylate kinase
14	425	36.6	215	2 S61843	adenylate kinase
15	424	36.5	215	2 G83184	adenylate kinase
16	419	36.1	224	2 B29792	adenylate kinase
17	419	36.1	241	2 JS0422	adenylate kinase
18	417	35.9	215	2 H90019	adenylate kinase
19	417	35.9	215	2 AB1777	adenylate kinase
20	416	35.8	248	2 S44765	adenylate kinase
21	415	35.7	229	2 JQ1944	adenylate kinase
22	413	35.6	214	2 AC0563	adenylate kinase
23	408	35.1	215	2 AC1401	adenylate kinase
24	407	35.1	215	2 H97282	adenylate kinase
25	405	34.9	214	1 K1ECA	adenylate kinase
26	405	34.9	214	2 C85545	adenylate kinase
27	405	34.9	214	2 G90694	adenylate kinase
28	401.5	34.6	214	2 C82255	adenylate kinase
29	401	34.5	217	2 JS0492	adenylate kinase

30	400	34.5	214	2 AG0378	adenylate kinase
31	395.5	34.1	217	2 D69334	adenylate kinase
32	395	34.0	222	2 T27960	hypothetical prote
33	393	33.9	206	2 G70307	adenylate kinase
34	389	33.5	199	2 PC4230	adenylate kinase
35	383.5	33.0	214	2 S70734	adenylate kinase
36	375	32.3	212	2 B95027	adenylate kinase
37	374	32.2	212	2 B97898	adenylate kinase
38	366.5	31.6	215	2 E8496	adenylate kinase
39	365.5	31.5	205	2 S50007	adenylate kinase
40	364	31.4	217	1 K1BSAF	adenylate kinase
41	355.5	30.6	220	2 G72247	adenylate kinase
42	352.5	30.4	220	2 F71052	probable adenylyate
43	346	29.8	215	2 E86884	adenylate kinase
44	343	29.5	220	2 E75090	adenylate kinase
45	340	29.3	215	2 S17987	adenylate kinase

## ALIGNMENTS

RESULT 1  
A34442  
nucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3, mitochondrial - bovine  
N:Alternate names: adenylyate kinase 3  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 15-Jun-1990 #sequence, revision 15-Jun-1990 #text, change 03-Jun-2002  
C/Accession: A34442; JH0512; A24201  
R:Yamada, M.; Shahjahan, M.; Tanabe, T.; Kishl, F.; Nakazawa, A.  
J. Biol. Chem. 264, 19192-19199, 1989  
A:Title: Cloning and characterization of cDNA for mitochondrial GTP:AMP phosphotrans  
A:Reference number: A34442; MUID:90037053; PMID:2478555  
A:Accession: A34442  
A:Molecule type: mRNA  
A:Residues: 1-227 <YAM>  
R:Shahjahan, M.; Yamada, M.; Tanaka, H.; Nakazawa, A.  
Gene 107, 313-317, 1991  
A:Title: Cloning and characterization of the gene encoding bovine mitochondrial adeny  
A:Reference number: JH0512; MUID:92084124; PMID:1748300  
A:Accession: JH0512  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-50 <SHA>  
R:romaselli, A.G.; Frank, R.; Schlitz, E.  
FEBS Lett. 202, 303-308, 1986  
A:Title: The complete primary structure of GTP:AMP phosphotransferase from beef heart  
A:Reference number: A24201; MUID:86248102; PMID:3013690  
A:Accession: A24201  
A:Molecule type: protein  
A:Residues: 2-10, 12-227 <TOM>  
C:Genetics:  
A:Gene: AK3  
A:Intons: 51/1; 91/1; 148/3; 188/2  
C:Superfamily: adenylyate kinase  
C:Keywords: ATP; mitochondrial; nucleotide binding; P-loop; phosphotransferase  
F:2-227/Product: GTP-AMP phosphotransferase, mitochondrial #status predicted <MAT>  
F:14-21/Region: nucleotide-binding motif A (P-loop)  
Query Match 94.0%; Score 1091; DB 2; Length 227;  
Best Local Similarity 91.6%; Pred. No. 5.8e-85;  
Matches 208; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPGSGKTVSSRTTTHFELKHLSSGDLRDNMTRGTEIGYAKAFI 60  
|||||  
DB 1 MGASARLLRAVIMGAPGSGKTVSSRTTTHFELKHLSSGDLRDNMTRGTEIGYAKAFI 60  
|||||  
QY 61 DQGLIPDDVWTRLVYHELNKLTQYSWLDGFPPTLPOAEALDRAVOIDPVINLVPEV 120  
|||||  
DB 61 DQGLIPDDVWTRLVYHELNKLTQYSWLDGFPPTLPOAEALDRAVOIDPVINLVPEV 120  
|||||  
QY 121 IKORTARWTHIPASGRYVNIENFNPKTGVGIDDLGEPFLIOREDDEPTVIKRLAYDQV 180  
|||||

Db 121 IKORLTAARMIHPGSGRVYNIENPPTKMGIDLTGEPVLQREDDRETVYKRLKAEADT 180  
Qy 181 KXVLYXOKKGVLEFSGTETNKIMPYVAFLOTQVPORSOKASVVP 227  
Db 181 EPLVLEYRRKKGVLEFSGTETNKIMPYVAFLOTQVPORSOKASVVP 227

RESULT 2  
J01945  
nucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3, mitochondrial - rat  
N:Alternate names: GTP-AMP phosphotransferase AK3  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 03-Jun-2002  
C:Accession: J01945  
R:Tanabe, T.; Yamada, M.; Noma, T.; Kajii, T.; Nakazawa, A.  
J. Biochem. 113, 200-207, 1993  
A:Title: Tissue-specific and developmentally regulated expression of the genes encoding  
A:Reference number: P00534; MUID:93224500; PMID:8468325  
A:Accession: J01945  
A:Molecule type: mRNA  
A:Residues: 1-227 <TAN>  
C:Cross-references: DDBJ:D13062; NID:g220797; PIDN:BAA02379.1; PID:g450312  
C:Superfamily: adenylylate kinase  
C:Keywords: ATP, GTP, mitochondrion, nucleotide binding, P-loop, phosphotransferase  
F:14-21/Region: nucleotide-binding motif A (P-loop)

Query Match 89.4%; Score 1038; DB 2; Length 227;  
Best Local Similarity 90.3%; Pred. No. 1.8e-80;  
Matches 205; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MGASARLRAVIMGAPGSGKGVSSRTTHFELKHLSSGDLRDNNLRGTETGLAKAFT 60  
Db 1 MGASGRLLRAVIMGAPGSGKGVSSRTTHFELKHLSSGDLRDNNLRGTETGLAKAFT 60

Qy 61 DOGKLTDDVMTRLAHEKNTLOYSWLIDGFPRTLPQAEALDRAVOIDTVINLNPFEV 120  
Db 61 DOGKLTDDVMTRLAHEKNTLOYSWLIDGFPRTLPQAEALDRAVOIDTVINLNPFEV 120

Qy 121 IKORLTAARMIHPGSGRVYNIENPPTKMGIDLTGEPVLQREDDRETVYKRLKAEADT 180  
Db 121 IKRLTAARMIHPGSGRVYNIENPPTKMGIDLTGEPVLQREDDRETVYKRLKAEADT 180

Qy 181 KXVLYXOKKGVLEFSGTETNKIMPYVAFLOTQVPORSOKASVVP 227  
Db 181 EPLVLEYRRKKGVLEFSGTETNKIMPYVAFLOTQVPORSOKASVVP 227

RESULT 3  
KIHUA3  
nucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3 - human  
N:Alternate names: adenylylate kinase 3  
C:Species: Homo sapiens (man)  
C:Date: 17-Apr-1993 #sequence\_revision 23-Mar-1995 #text\_change 03-Jun-2002  
C:Accession: A42820; S16381  
R:Xu, G.; O'Connell, P.; Stevens, J.; White, R.  
Genomics 13, 537-542, 1992  
A:Title: Characterization of human adenylylate kinase 3 (AK3) cDNA and mapping of the AK3  
A:Reference number: A42820; MUID:92347846; PMID:1639383  
A:Accession: A42820  
A:Molecule type: mRNA  
A:Residues: 1-223 <XUG>  
A:Cross-references: EMBL:X60673; NID:g28576; PIDN:CAA43088.1; PID:g28577; GB:S41502  
A:Experimental source: frontal-cortex  
A:Note: sequence extracted from NCBI backbone (NCBIN:109644, NCBI:P109645)  
C:Comment: This isoform is found in the mitochondrial matrix.  
C:Genetics:  
A:Gene: GDB:AK3  
A:Cross-references: GDB:118988; OMTW:103030  
A:Map position: 9pter-9p13  
C:Function:  
A:Description: catalyzes the reversible phosphorylation of adenine monophosphate with nu  
A:Note: GTP is preferred to ATP as a substrate  
C:Superfamily: adenylylate kinase

C:Keywords: ATP, mitochondrial matrix, mitochondrion, P-loop, phosphotransferase  
F:12-19/Region: nucleotide-binding motif A (P-loop) #status atypical  
F:85-89/Region: nucleotide-binding motif B #status atypical  
F:22,33,35,88/Active site: Cys, His, Ser, Asp #status predicted

Query Match 60.3%; Score 700.5; DB 1; Length 223;  
Best Local Similarity 58.8%; Pred. No. 6.2e-52;  
Matches 130; Conservative 38; Mismatches 52; Indels 1; Gaps 1;

Qy 4 SARLRAVIMGAPGSGKGVSSRTTHFELKHLSSGDLRDNNLRGTETGLAKAFTDGG 63  
Db 2 ASKLLRAVIMGAPGSGKGVSSRTTHFELKHLSSGDLRDNNLRGTETGLAKAFTDGG 61

Qy 64 KLTPDDVMTRLAHEKNTLOYSWLIDGFPRTLPQAEALDRAVOIDTVINLNPFEV 123  
Db 62 LTPDDVMTRLAHEKNTLOYSWLIDGFPRTLPQAEALDRAVOIDTVINLNPFEV 121

Qy 124 RLTARMIHPGSGRVYNIENPPTKMGIDLTGEPVLQREDDRETVYKRLKAEADT 183  
Db 122 RLSRRMIHPGSGRVYNIENPPTKMGIDLTGEPVLQREDDRETVYKRLKAEADT 181

Qy 184 LXVYXOKKGVLEFSGTETNKIMPYVAFLOTQVPORSOKA 223  
Db 182 IELYSRGVLDHPSGTETNKIMPYVAFLOTQVPORSOKA 222

RESULT 4  
I64062  
adenylate kinase (EC 2.7.4.3) - Haemophilus influenzae (strain Rd KW20)  
N:Alternate names: ATP-AMP phosphotransferase  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 18-Jun-1999  
C:Accession: I64062; S15290  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage  
; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.T.; Glodek, A.; Kelley, J.M.; Weidman  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:9550630; PMID:7542800  
A:Accession: I64062  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-214 <TIGR>  
A:Cross-references: GB:U32719; GB:I42023; NID:g1573310; PIDN:AAC22010.1; PID:g1573319  
A:Experimental source: strain Rd KW20  
R:Maekell, D.J.; Szabo, M.J.; Butler, P.D.; Williams, A.E.; Moxon, E.R.  
Mol. Microbiol. 5, 1013-1022, 1991  
A:Title: Molecular analysis of a complex locus from Haemophilus influenzae involved in  
A:Reference number: S15287; MUID:92065797; PMID:1956282  
A:Accession: S15290  
A:Molecule type: DNA  
A:Residues: 1-77, 'A', '79-214 <MAS>  
A:Cross-references: EMBL:X57315; NID:g43587; PIDN:CAA40570.1; PID:g43591  
A:Experimental source: strain RM704  
C:Genetics:  
A:Gene: adh  
C:Function:  
A:Note: magnesium required  
C:Superfamily: adenylylate kinase  
C:Keywords: ATP, monomer, P-loop, phosphotransferase  
F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical  
F:80-85/Region: nucleotide-binding motif B #status atypical  
F:30,84/Active site: Ser, Asp #status predicted

Query Match 38.5%; Score 447.5; DB 2; Length 214;  
Best Local Similarity 46.1%; Pred. No. 1.5e-30;  
Matches 95; Conservative 37; Mismatches 61; Indels 13; Gaps 4;

Qy 8 LRAVIMGAPGSGKGVSSRTTHFELKHLSSGDLRDNNLRGTETGLAKAFTDGG 67  
Db 1 KRIILGAPGAGGTQAOEITMKFGIPQISTDGMRAATKAGTELGKAKALMDSEKLPV 60

```

Oy 68 DO-----VMTLALHEKLNLTQYSWLDDGFPRTLPOAQL-DRAVQIDVTYNLNEPEVI 121
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 61 DELVALVAKDXIAQADCTN-----GFLDDGFPRTLPOADALDGSYKIDLEFDVDPDEVI 116

Oy 122 KQRLTARNIHPSASGRVNIIEFNPPKTVGIDDLTGEPLLQREDDKPEYIKLKAVEDQTK 181
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 117 VERMSGRVHVASGRSHYIYVNPVKVEKGDDVTGSDLLITRADDKREYTLDSLAVYHNKQTS 176

Oy 182 XLVLYTQ---KKGVLETFPSGTETNKI 204
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 177 PLIDYQAQAKAAGNTQYERLDDGTVK 202

RESULT 5
S23568
adenylate kinase (EC 2.7.4.3) ADK2 - yeast (Saccharomyces cerevisiae)
N/Alternate names: PAK3 protein; protein YER170W
C/Species: Saccharomyces cerevisiae
C/Date: 12-Mar-1993 #sequence, revision 12-Mar-1993 #text, change 19-Jan-2001
C/Accession: S23568; JCI135; S50673
R/Schlicker, R.; Magdalen, V.; Bandlow, W.
MOL. Gen. Genet. 233, 363-371, 1992
A/Title: A new member of the adenylate kinase family in yeast: PAK3 is highly homologous
A/Reference number: S23568; MUID:92318888; PMID:1620094
A/Accession: S23568
A/Molecule type: DNA
A/Residues: 1-225 <SOCH>
A/Cross-references: EMBL:X65126; NID:g40936; PIDN:CAA46254.1; PID:g4097
R/Cooper, A.J.; Friedberg, E.C.
C/Date: 114, 145-148, 1992
A/Title: A putative second adenylate kinase-encoding gene from the yeast Saccharomyces
A/Reference number: JCI135; MUID:92267376; PMID:1587477
A/Accession: JCI135
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-225 <COO>
A/Cross-references: GB:M7757; NID:g171045; PIDN:AAA34418.1; PID:g171046
R/Dietrich, F.S.
A/Description: The sequence of S. cerevisiae cosmid 9163 and 9132.
A/Reference number: S50673
A/Accession: S50673
A/Molecule type: DNA
A/Residues: 1-225 <DIE>
A/Cross-references: EMBL:U18922; NID:g603405; PIDN:AAB64697.1; PID:g603411. MIPS:YER170W
C/Genetics:
A/Gene: SGD:ADK2; PAK3
A/Cross-references: SGD:S0000972; MIPS:YER170W
A/Map position: 5R
C/Function:
A/Description: phosphotransferase
A/Superfamily: adenylate kinase
C/Keywords: ATP; mitochondrion; nucleotide binding; P-loop; phosphotransferase
C/21-28/Region: nucleotide-binding motif A (P-loop)

Query Match 37.9%; Score 439.5; DB 2; Length 225;
Best Local Similarity 44.9%; Pred. No. 7, 66-30;
Matches 93; Conservative 37; Mismatches 66; Indels 11; Gaps 4;

Oy 8 LRAVIMGAPSGKGTSSRTTTH-ELKHSSGDLRLDNMLRGTEIGVLAFAFDQGLI 66
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 15 LRLILGAPGSGKGTQTSRLKQIPQLSSISSGDLRQEIKSESTLGGREATTYINQKLL 74

Oy 67 PDDVWTRLALHEKNL-----TOYSLDDGFPRTLPOAALDRAYO-----IDVTYNLNV 117
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 75 PDDLTLTRTLRSLALGLKPSAMWLDGFPRTTAQAASALDELKQNDASLNLVVELDVP 134

Oy 118 FEVIKQRLTARNIHPSASGRVNIIEFNPPKTVGIDDLTGEPLLQREDDKPEYIKLKAWE 177
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 135 ESTILIERENKYNVHPSGRVNIYVNPVKVEKGDDVTGSDLLITRADDKREYTLDSLAVYHNKQTS 194

Oy 178 DQTKXVLXYQKGVLETFPSGTETNKI 204

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Db      195   KTNPELKDYYKKSGIFGTGVS-ETSDI 220
          : ||::|::| | | | |
RESULT 6
T44404
adenylate kinase (EC 2.7.4.3) [imported] - Bacillus halodurans
C:Species: Bacillus halodurans
C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 15-Jun-2001
C:Accession: T44404; C83669
R:Takami, H.; Takaki, Y.; Nakasone, K.; Hirama, C.; Inoue, A.; Horikoshi, K.
Biocel. Biotechnol. Biochem. 65, 452-455, 1999
A>Title: Sequence analysis of a 3.3-kb region including the major ribosomal protein gene
A:Reference number: 222756; MUID:99209008; PMID:10192928
A:Accession: T44404
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-217 <STO>
A:Cross-references: EMBL:AB017508; NID:g4512395; PIDN:BAA75292.1; PID:g4512425
A:Experimental source: strain C-125
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: C83669
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-217 <STO>
A:Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BAB03874.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: adk
A:Superfamily: adenylate kinase
C:Keywords: phosphotransferase
Query Match           37.6%; Score 437; DB 2; Length 217;
Best Local Similarity 42.7%; Pred. No. 1,2e-29;
Matches 85; Conservative 47; Mismatches 61; Indels 6; Gaps 2;
 Oy    8 LRAVIMAGPGSGKGVTSRRITTFELKLHSSGDLLRDNMRLGTETIGVLAKAFIDQGLIP 67
       1 ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
 Db     1 NMLILMGPBGAGCTQAETKEIKYGIPIHSIGDMFRAMKNMETELGAKASYMDAGEIIVP 60
 Oy    68 DDVMTRLALHEL-KNLIDYSWLDGFPRTLQAEALDRAY-----QIDTYINLVPREVI 121
       1::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
 Db     61 DEVTIGIYRDLISODDCONGFLDGFPRTVQAQEALEDEITASLDKKLDYVINIDVPQL 120
       1::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
 Oy    122 KORLARMIHPASGRVNIIEFNPKRTVGIDLTGEPLIQREDDKPETYIKRLKAIEDQT 181
        |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
 Db    121 MDRLRGVRVPTSGRTYIVIFNPKEVICGVDSSELQRDDDKPEYTKRLLEVNRQAQ 180
 Oy    182 XLVXLYOKKVLETFSGTE 200
       ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
 Db    181 PLIDFYSEKGYLONINGDO 199
       ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 7
S31338
adenylate kinase (EC 2.7.4.3) 1 - fission yeast (Schizosaccharomyces pombe)
N:Alternate names: ATP-AMP transphosphorylase
C:Species: Schizosaccharomyces pombe
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Dec-1999
C:Accession: A46718; T38862; S31338
R:Konrad, M.
J. Biol. Chem. 268, 11326-11334, 1993
A>Title: Molecular analysis of the essential gene for adenylate kinase from the fissi
A:Reference number: A46718; MUID:93266590; PMID:8496185
A:Accession: A46718
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <KO2>
A:Cross-references: EMBL:X70363; NID:g95535; PIDN:CAA49826.1; PID:g95536
A>Note: sequence extracted from NCBI backbone (NCBIN:132838, NCBI:P.132839)
```





## RESULT 9

JCS893

adenylate kinase (EC 2.7.4.3) 2B - human

N:Alternate names: ATP-AMP transphosphorylase

C:Species: Homo sapiens (man)

C:Date: 18-Mar-1998 #sequence\_revision 18-Mar-1998 #text\_change 18-Jun-1999

C:Accession: JCS893

R:Lee, Y.; Kim, J.W.; Lee, S.M.; Kim, H.J.; Lee, K.S.; Park, C.; Choe, I.S.

J. Biochem. 123, 47-54, 1998

A:Title: Cloning and expression of human adenylate kinase 2 isozymes: Differential expre

A:Reference number: JCS893; MUID:98162934; PMID:9504408

A:Cross-references: GB:U54645; NID:q171086; PIDN:AAC13881.1; PID:q1477653

A:Experimental source: tissue fetal liver

C:Comment: This key enzyme is involved in energy metabolism.

C:Genetics:

A:Gene: ack2b

C:Function:

A:Note: magnesium required

C:Superfamily: adenylate kinase

C:Keywords: alternative splicing; ATP; P-loop; phosphotransferase

F:22-29/Region: nucleotide-binding motif A (P-loop) #status atypical

F:95-100/Region: nucleotide-binding motif B #status atypical

F:42-92/Disulfide bonds: #status predicted

F:43,99,145/Active site: His, Asp, His #status predicted

Query Match

Best local similarity 37.1%; Score 431; DB 2; Length 232;

Matches 87; Conservative 45; Mismatches 62; Indels 6; Gaps 2;

Db 8 LRAVIMAPSGKCTVSSRTTHHELMKHSGLLRNMLRGTEIGVLAFAFDGKLP 67

Db 16 IRAVLGPAGKGTQAPRLAENPCVCHLATGMLRAMVAGSLGKRLKATMDAGKLV 75

QY 68 DDVWTRLALHELNK-LTQYSMLDGFPPRTLPQAEALD-----RAYQIDTYINLWPREVI 121

Db 76 DENWVELLEKNLEPLKNGFLDGFRTYQAEMLDLEKREKIDSYIESIPDLSL 135

QY 122 KQRLTARMIHPASGRVNIENFPKRTVIGDILGEPPIQREDDKPETVIRKLKAYEDQTK 181

Db 136 IRRITGRILHPKSGRSYHEEFNPKPEKMDITGEPLIRSDDEKALKIRLQAYHYQT 195

QY 182 XVLXYOKKGVLETFSGTER 201

Db 196 PLIEYRKRGIHSAIDASQ 215

## RESULT 10

G02248

adenylate kinase (EC 2.7.4.3) 2 - human

N:Alternate names: ATP-AMP transphosphorylase

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 18-Jun-1999

C:Accession: G02248

R:Choe, I.

submitted to the EMBL Data Library, November 1995

A:Reference number: H00907

A:Accession: G02248

A:Status: preliminary; translated from GB/EMBL/DDDB

A:Molecule type: mRNA

A:Residues: 1-239 &lt;CHO&gt;

A:Cross-references: EMBL:U3945; NID:g1209686; PIDN:AAC52061.1; PID:g1209687

A:Experimental source: tissue fetal liver

-7 44 11 116" data-label="Text"&gt;C:Genetics:

-19 44 -7 116" data-label="Text"&gt;A:Gene: ack2

-31 44 -19 116" data-label="Text"&gt;C:Function:

-43 44 -31 488" data-label="Text"&gt;A:Note: magnesium required

-55 44 -43 488" data-label="Text"&gt;C:Superfamily: adenylate kinase

-67 44 -55 488" data-label="Text"&gt;C:Keywords: ATP; P-loop; phosphotransferase

-79 44 -67 488" data-label="Text"&gt;F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical

-91 44 -79 488" data-label="Text"&gt;F:80-85/Region: nucleotide-binding motif B #status atypical

-103 44 -91 488" data-label="Text"&gt;F:30,84,126/Active site: Ser, Asp, His #status predicted

F:22-29/Region: nucleotide-binding motif A (P-loop) #status atypical

F:95-100/Region: nucleotide-binding motif B #status atypical

F:42-92/Disulfide bonds: #status predicted

F:43,99,145/Active site: His, Asp, His #status predicted

Query Match

Best local similarity 37.1%; Score 431; DB 2; Length 239;

Matches 87; Conservative 45; Mismatches 62; Indels 6; Gaps 2;

QY 8 LRAVIMAPSGKCTVSSRTTHHELMKHSGLLRNMLRGTEIGVLAFAFDGKLP 67

Db 16 IRAVLGPAGKGTQAPRLAENPCVCHLATGMLRAMVAGSLGKRLKATMDAGKLV 75

QY 68 DDVWTRLALHELNK-LTQYSMLDGFPPRTLPQAEALD-----RAYQIDTYINLWPREVI 121

Db 76 DENWVELLEKNLEPLKNGFLDGFRTYQAEMLDLEKREKIDSYIESIPDLSL 135

QY 122 KQRLTARMIHPASGRVNIENFPKRTVIGDILGEPPIQREDDKPETVIRKLKAYEDQTK 181

Db 136 IRRITGRILHPKSGRSYHEEFNPKPEKMDITGEPLIRSDDEKALKIRLQAYHYQT 195

QY 182 XVLXYOKKGVLETFSGTER 201

Db 196 PLIEYRKRGIHSAIDASQ 215

## RESULT 11

S61841

adenylate kinase (EC 2.7.4.3) [similarity] - Neisseria meningitidis (strain 22491 ser

N:Alternate names: ATP-AMP transphosphorylase

C:Species: Neisseria meningitidis

A:Variety: strain P63; ATCC 43831

C:Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 02-Feb-2001

C:Accession: S61841; S61842; F81951

R:Valquez, J.A.; Barron, S.; O'Rourke, M.; Carpenter, G.; Fell, E.; Smith, N.H.; Spr

Mol. Microbiol. 15, 1001-1007, 1995

A:Title: Interspecies recombination in nature: a meningococcus that has acquired a g

A:Reference number: S61840; MUID:95349386; PMID:7623657

A:Accession: S61841

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-215 &lt;VAO&gt;

A:Cross-references: EMBL:L36470; NID:g845613; PIDN:AA99173.1; PID:g845614

A:Experimental source: ATCC 43831

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mc

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491J19

A:Reference number: A81775; MUID:2022556; PMID:10761919

A:Accession: F81951

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-215 &lt;PAR&gt;

A:Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84301.1; PID:g737

A:Experimental source: serogroup A, strain 22491

C:Genetics:

A:Gene: ack

C:Function:

A:Note: magnesium required

C:Superfamily: adenylate kinase

C:Keywords: ATP; P-loop; phosphotransferase

F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical

F:80-85/Region: nucleotide-binding motif B #status atypical

F:30,84,126/Active site: Ser, Asp, His #status predicted

Query Match	37.0%;	Score 430;	DB 2;	Length 215;
Best Local Similarity	-45.7%;	Pred. NO. 4.6e-29;		
Matches 86;	Conservative 40;	Mismatches 52;	Indels 10;	Gaps 3

```
QY      8 DDMV-----TRLALHELNLTQYSWMLDGFPRTLPOAEAL-DRAVOIDVTINLVNPFVEY   121
        |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      61 DDIIIGMWKEHRIADDDCKN---GFLFDGFPRTLAQAEMEAEGVDLDAAVEIDVPDSVI   116

QY      122 KQRLTARNIHASGRVYNIEFNPRTKYGIDDLTGEPPLIQREDDKAPETIYIKKLAYEDOTK   181
        |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      117 VDRSGRGVRVHLASGRTHVYNPNPKVEKGDDVTGEDLIQRDDDKEEFYKKRLRAYVHEOTE   176

QY      182 XVLXYYOK 189
        :::|:::|
Db     177 VLVDIFYSK 184
```

RESULT 12  
F81154

adenylylate kinase *MMB0823* (imported) - *Neisseria meningitidis* (strain MC58 serogroup B)  
C:Species: *Neisseria meningitidis*  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: F81154  
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.R.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; White, H.; Qiu, H.; Vamthyan, V.; Gill, J.; Scarlato, V.; Maignan, V.; Plaza, M. Science 287, 1809-1815, 2000  
A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vett  
A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
A:Reference number: A81000; MIMD:2015755; PMID:10710307  
A:Accession: F81154  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-215 <RET>  
A:Cross-references: GB:AE002435; GB:AE002098; NID:g72226049; PIDN:AAE41236.1; PID:g72226050  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: MMB0823  
A:Superfamily: adenylylate kinase

Query Match	37.0%;	Score 430;	DB 2;	Length 215;
Best Local Similarity	45.7%;	Pred. NO. 4.6e-29;		
Matches	86;	Conservative	40;	Mismatches 52;
			Indels	10;
			Gaps	3;

Dd	1	MAKALLCAGPAGCKTQAFITPAFGIPQISTGDMRLRAIKAGTFLGLEAKIIDEGGLVR	60
Qy	68	DDVW-----TRLALHEKLNLTQYSMLDDGFPRTLPQAEAL-DRAYQIDTYINLVNPREEVI	121
Dd	61	DDILIGWKEKELIADDCKN---GFLFDGFPRTLAQAEAMAEAGVDADVAVEIDVPSVI	116
Qy	122	KQRLTARMIHPASGRVYNIEENPKPTVGIDLTGEPFLQREDKPEFYIKRLKAYEDOTK	181
Dd	117	VDRKSGRVHLASRGLTHVYINPNPKVEGSKDVGTEGDLIQRDDKDEEYIKKRLAYVHEQTE	176
Qy	182	XVLXYYOK	189
Dd	177	VLVDEYSK	184

### RESULT 13

C:adenylylate kinase (EC 2.7.4.3) - Bordetella pertussis  
N:alternate names: ATP-AMP transphosphorylase  
C:species: Bordetella pertussis  
C:date: 07-Sep-1994 #sequence\_revision 10-Nov-1995 #text\_change 18-Jun-1999  
#accession: S43016

R.Gillies, A.M., Sismelro, O.; Munier, H., Feblian, H.; Mantsch, H.H.; Surewicz, W.K.; Eur. J. Biochem. 218, 921-927, 1993  
A>Title: Structural and physico-chemical characteristics of Bordetella pertussis aden  
A,Reference number: S43016; MUID:94109391; PMID:8201944

Query Match	36.98;	Score 428;	DB 2;	Length 218;
Best Local Similarity	42.18;	Pred. No. 6.9e-29;		
Matches 85; Conservative	45;	Mismatches 64;	Indels 8;	Gaps 3;

[illegible]

RESULT 14

adenylate kinase (EC 2.7.4.3) - *Neisseria gonorrhoeae* (strain CH-95)  
N:Alternate names: AMP-AMP transphosphorylase  
C:Species: *Neisseria gonorrhoeae*  
A:Variety: strain CH-95  
C:Date: 27-Apr-1996 #sequence-revision 13-Mar-1997 #text-change 18-Jun-1999  
C:Accession: S61843  
R:Vazquez, J.A.; Berron, S.; O'Rourke, M.; Carpenter, G.; Fell, E.; Smith, N.H.; Spr  
Mol. Microbiol. 1, 1001-1007, 1995  
A:Title: Interspecies recombination in nature: a meningococcus that has acquired a go  
A:Reference number: S61840; MUID:95349386; PMID:7623657  
A:Accession: S61843  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-215 (AAZ>  
A:Cross-references: EMBL:L36471; NID:G845615; PIDN:AAA9174.1; PID:G845616  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995  
C:Superfamily: adenylyate Kinase  
C:Keywords: AMP; P-loop; phosphotransferase  
F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical  
F:80-85/Region: nucleotide-binding motif B #status atypical  
F:30,84,126/Active site: Ser, Asp, His #status predicted

Query Match	36.6%	Score 425;	DB 2;	Length 215;
Best Local Similarity	45.7%;	Pred. No. 1.2e-28;		
Matches	86;	Conservative	40;	Mismatches 52; Indels 10; Gaps 3;

Oy 8 LRAVIMGAPSGCKGYSSRITTHFELKHSSGDLRLDMLEKTEIGVAKAFIDGKLP 67  
 :::::||||| : || : ::||| : || : || ||| :  
 Db 1 MKALLGAPGAGKGTQAFITAFGIPIQSTGDMRAAIKAGTPLGLEAKKIIDEGLVR 60

```

QY 68 DDVM-----TRLALHELKLNLTQYSMLLDGFPRTLPOAEAL-DRAYQIDFYINLVPEFY 121
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 61 DDILIGMVKERINQDDCKN-----GFLFDGFPRTLQAEMAVENGVLDAVEIDVSDSYI 116
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 122 KORLTRKRWIHPASGRVYNIENFPKTVGIDDLTGEPLIQREDDKPEYIKRLKAYEDQTK 181
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 117 VDRMSGRRVHLASGRYVHTYNPPTKTEGKDDVTGEDLIQRDDDKETVKKRLAVYHQTE 176
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 182 XVLYXYXQK 189
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 177 VLVDFTYSK 184
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

```

## RESULT 15

```

G83184
adenylate kinase PA3686 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83184
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Berman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G83184
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-215 <STO>
A:Cross-references: GB:AE004788; GB:AE004091; NID:g9949846; PIDN:AAG07074.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: adk; PA3686
C:Superfamily: adenylate kinase

```

```

Query Match          36.5%; Score 424; DB 2; Length 215;
Best Local Similarity 46.6%; Pred. No. 1.5e-28;
Matches 88; Conservative 29; Mismatches 70; Indels 2; Gaps 2;

```

```

QY 8. LRAVINGAPGSGKGVSSRTTTHFELKHLSSGDLRDNMIRGTEIGVLAFAITDQGLIP 67
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 1 MRVILGAPGAGAGTGARFITEKFIPOISTGDMLEAAVAGSPLGQOVGVMDSGLVS 60
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 68 DDVMTRLALHELKLNLTQYSMLLDGFPRTLPOAEAL-DRAYQIDFYINLVPEFYKQRL 125
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 61 DDITIALIKERTHEADCAKGFLEDFPRTIPQAEALKDAGVTTDHAVEIAVDDDEIVSRI 120
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Y 126 TARWHPASGRVYNIENFPKTVGIDDLTGEPLIQREDDKPEYIKRLKAYEDQTKXVLYK 185
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 121 AGRVHVPASGRVYHTENPFRKAGKDVGTGEELIQREDDKEETVRRHRLSVYHSQTKPLVD 180
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 186 YVOKKGVLE 194
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 181 FYOKLSAAE 189
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

```

Search completed: March 19, 2003, 16:44:32  
 Job time : 694 secs

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OY 122 KORLTARWHPASGRVYNIEFNPKTVGIDDLTGEPLIQEDDKPEYVIRKLKAYEDQK 181
DB 121 KORLTARWHPASGRVYNIEFNPKTVGIDDLTGEPLIQEDDKPEYVIRKLKAYEDQK 180
OY 182 XVLXYOKKGVLETFSGTETNKIMPYVAFLOTKVPORSOKASVTP 227
DB 181 PULEYTRKKGVLETFSGTETNKIMPYVAFLOTKVPORSOKASVTP 226

RESULT 2
KAD3_BOVIN STANDARD; PRT; 226 AA.
AC P08760;
DT 01-NOV-1988 (rel. 09, Created)
DT 01-APR-1990 (rel. 14, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last annotation update)
DE GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3).
GN AK3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90037053; PubMed=2478555;
RA Yamada M., Shahjahan M., Tanabe T., Kishi F., Nakazawa A.;
RT "Cloning and characterization of cDNA for mitochondrial GTP:AMP
RT phosphotransferase of bovine liver."
RL J. Biol. Chem. 264:19192-19199(1989).
RN [2]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=86248102; PubMed=3013690;
RA Tomasselli A.G., Frank R., Schiltz E.;
RT "The complete primary structure of GTP:AMP phosphotransferase from
RT beef heart mitochondria."
RL FEBS Lett. 202:303-308(1986).
RN [3]
RP SEQUENCE OF 1-49 FROM N.A.
RA MEDLINE=92084124; PubMed=1748300;
RA Shahjahan M., Yamada M., Tanaka H., Nakazawa A.;
RT "Cloning and characterization of the gene encoding bovine
RT mitochondrial adenylate kinase isozyme 3."
RL Gene 107:313-317(1991).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=91084487; PubMed=2175649;
RA Diederichs K., Schulz G.E.;
RT "Three-dimensional structure of the complex between the mitochondrial
RT matrix adenylate kinase and its substrate AMP."
RL Biochemistry 29:8138-8144(1990).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
RX MEDLINE=91132661; PubMed=1994037;
RA Diederichs K., Schulz G.E.;
RT "The refined structure of the complex between adenylate kinase from
RT beef heart mitochondrial matrix and its substrate AMP at 1.85-A
RT resolution."
RL J. Mol. Biol. 217:541-549(1991).
CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@sib-sib.ch).
CC -----

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```

DR EMBL: D10376; BAA01210.1; -.
DR EMBL: D10373; BAA01210.1; JOINED.
DR EMBL: D10374; BAA01210.1; JOINED.
DR EMBL: D10375; BAA01210.1; JOINED.
DR EMBL: M25757; AAA30705.1; -.
DR PIR: A24201; A24201.
DR PIR: A34442; A34442.
DR PIR: JH0512; JH0512.
DR PDB: 2AK3; 12-MAY-95.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW Transferase; Kinase; GTP-binding; Mitochondrion; 3D-structure.
FT INIT MET 0
FT NP_BIND 13 21 GTP (BY SIMILARTY).
FT CONFLICT 10 10 MISSING (IN REF. 2).
FT STRAND 8 12
FT TURN 15 16
FT HELIX 19 29
FT STRAND 33 36
FT HELIX 37 45
FT TURN 46 48
FT HELIX 50 60
FT TURN 61 62
FT HELIX 67 79
FT TURN 80 81
FT STRAND 86 89
FT TURN 95 102
FT HELIX 103 104
FT STRAND 109 114
FT HELIX 117 124
FT TURN 125 125
FT STRAND 127 130
FT TURN 131 134
FT STRAND 135 138
FT TURN 139 141
FT STRAND 142 142
FT TURN 147 148
FT STRAND 149 149
FT TURN 151 153
FT STRAND 156 156
FT STRAND 158 158
FT TURN 161 162
FT HELIX 165 189
FT TURN 190 190
FT STRAND 192 196
FT HELIX 200 212
FT TURN 213 214
SQ SEQUENCE 226 AA; 25540 MW; 2B74C2FBAAA7CBA9 CRC64;

Query Match 93.5%; Score 1086; DR 1; Length 226;
Best Local Similarity 91.6%; Pred. No. 1,5e-86;
Matches 207; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

```



```

RESULT 3
KAD3_MOUSE
ID KAD3_MOUSE STANDARD: PRT: 219 AA.
AC Q9WTP7: 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3)
DE (Fragment)
GN AK3 OR AK-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBL_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Noma T.;
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AB020203; BAA77360.1; -
CC DR HSSP: P08760; 2AK3.
CC DR MGD: MGI:87979; AK3.
CC DR InterPro: IPR000850; Adenylate_kin.
CC DR Pfam: PF00406; adenylatekinase.1.
CC DR PRINTS: PR00094; ADENYLTKINASE.
CC DR PRODOM: PD000657; Adenylate_kin.1.
CC DR PROSITE: PS00113; ADENYLATE_KINASE.1.
CC KW Transferase; kinase; GTP-binding; Mitochondrion.
CC FT NON_TER 1
CC FT NP_BIND 6 14 GTP (BY SIMILARITY).
CC SQ SEQUENCE 219 AA; 24640 MW; 7DDB8DFA2C0EE7C5 CRC64;

Query Match 90.1%; Score 1046; DB 1; Length 219;
Best Local Similarity 92.2%; Pred. No. 4e-83;
Matches 202; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

OY 9 RAVINGAPSGSGKTVSSRTTHFEELKHLSSGDLRLDNMLRGTEIGYLAFAFIIDGKLIID 68
DB 1 RAVINGAPSGSGKTVSSRTTHFEELKHLSSGDLRLDNMLRGTEIGYLAFAFIIDGKLIID 60
OY 69 DWETRLALHELKNTQYSWLDGFPRTLPOAEALDRAVQIDIVINLVPEFVIKORLTAR 128
DB 61 DWETRLALHELKNTQCSWLDGFPRTLPOAEALDRAVQIDIVINLVPEFVIKORLTAR 120
OY 129 WTHPASGRVYNIEFNPVKTVGIDDLTGEPILQREDKPEFVIKRLKAYEDQTXVLYXVQ 188
DB 121 WTHPASGRVYNIEFNPVKTVGIDDLTGEPILQREDKPEFVIKRLKAYEDQTXVLYXVQ 180
OY 189 KKGVLTEFSGTEFNKIMPVYVAFLOTKVPORSOKASVTP 227
DB 181 KKGVLTEFSGTEFNKIMPVYVAFLOTKVPORSOKASVTP 219

RESULT 4
KAD3_RAT
ID KAD3_RAT STANDARD: PRT: 226 AA.
AC P29411:
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3).

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GN AK3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBL_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanabe T., Yamada M., Noma T., Kajii T., Nakazawa A.;
RT "Tissue-specific and developmentally regulated expression of the
RT gene encoding adenylate kinase isozyemes."
RL J. Biochem. 113:200-207(1993).
CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D13062; BAA02379.1; -
CC DR PIR: J01945; J01945.
CC DR HSSP: P08760; 2AK3.
CC DR InterPro: IPR000850; Adenylate_kin.
CC DR Pfam: PF00406; adenylatekinase.1.
CC DR PRINTS: PR00094; ADENYLTKINASE.
CC DR PRODOM: PD000657; Adenylate_kin.1.
CC DR PROSITE: PS00113; ADENYLATE_KINASE.1.
CC KW Transferase; kinase; GTP-binding; Mitochondrion.
CC FT INIT_MET 0
CC FT NP_BIND 13 21 GTP (BY SIMILARITY).
CC SQ SEQUENCE 226 AA; 25307 MW; D57FE37404AA6625 CRC64;

Query Match 89.0%; Score 1033; DB 1; Length 226;
Best Local Similarity 90.3%; Pred. No. 5.4e-82;
Matches 204; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

OY 2 GASARLLRAVIMAPSGSGKTVSSRTTHFEELKHLSSGDLRLDNMLRGTEIGYLAFAFIID 61
DB 1 GASARLLRAVIMAPSGSGKTVSSRTTHFEELKHLSSGDLRLDNMLRGTEIGYLAFAFIID 60
OY 62 OGKLIIPDDVTRLALHELKNTQYSWLDGFPRTLPOAEALDRAVQIDIVINLVPEFVI 121
DB 61 OGKLIIPDDVTRLALHELKNTQCSWLDGFPRTLPOAEALDRAVQIDIVINLVPEFVI 120
OY 122 KORLTARWTHPASGRVYNIEFNPVKTVGIDDLTGEPILQREDKPEFVIKRLKAYEDQTX 181
DB 121 KORLTARWTHPASGRVYNIEFNPVKTVGIDDLTGEPILQREDKPEFVIKRLKAYEDQTX 180
OY 182 XVLXYXVQKKGVLTEFSGTEFNKIMPVYVAFLOTKVPORSOKASVTP 227
DB 181 XVLXYXVQKKGVLTEFSGTEFNKIMPVYVAFLOTKVPORSOKASVTP 226

RESULT 5
KAD4_MOUSE
ID KAD4_MOUSE STANDARD: PRT: 223 AA.
AC Q9WUR9: 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (ATP-AMP
DE transphosphorylase).
GN AK4 OR AK-4 OR AK3B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBL_TaxID=10090;

```

```
DE Adenylylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (ATP-AMP  
transphosphorylase).  
GN AK4.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI_Taxid=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Miscar; TISSUE=Forebrain;  
RX MEDLINE=99033072; PubMed=9813319;  
RA Yoneda T., Sato M., Maeda M., Takagi H.;  
RT Identification of a novel adenylylate kinase system in the brain:  
cloning of the fourth adenylylate kinase.*;  
RL Brain Res. Mol. Brain Res. 62:187-195(1998).  
CC CC -1- CATALYTIC ACTIVITY: GTP + AMP = GDP + ADP.  
CC CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (Potential).  
CC CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE PYRAMIDAL CELLS IN THE  
HIPPOCAMPUS.  
CC CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE CENTRAL NERVOUS SYSTEM IN A  
REGION-SPECIFIC MANNER FROM THE MIDDLE STAGE OF EMBRYOGENESIS TO  
THE ADULTHOOD IN THE RODENT.  
CC CC -1- SIMILARITY: BELONGS TO THE ADENYLYLATE KINASE FAMILY.  
-----  
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-----  
CC EMBL; D87809; BAA7761.1; .  
DR HSSP; P08760; 2AK3.  
DR InterPro; IPR000850; Adenylylate_kin.  
DR Pfam; PF00406; adenylylatekinase. 1.  
DR PRINTS; PR00094; ADENYLTKINASE.  
DR PRODOM; PD000657; Adenylylate_kin; 1.  
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.  
KW transferase; Kinase; GTP-binding; Mitochondrion.  
NP_BIND 12 20 GTP (BY SIMILARITY).  
FT FT  
SQ SEQUENCE 223 AA; 25203 MW; B5A9BB45CEFA3C19B CRC64;
```

GN AK4 OR AK3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92347846; PubMed=1639383;  
RA Xu G., O'Connell P., Stevens J., White R.;  
RT "Characterization of human adenylate kinase 3 (AK3) cDNA and mapping  
RL Genomics 13:537-542(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC Tissue=Lung;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.  
CC -1- SUBUNIT: MONOMER.  
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
CC -----  
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CC -----  
DR EMBL; X60673; CAA43088.1; -.  
DR EMBL; BC016180; AAH16180.1; -.  
DR PIR; S16381; S16381.  
DR PIR; S16380; S16380.  
DR PIR; A42820; A42820.  
DR HSP; P08760; ZAK3.  
DR Genew; HGNC:363; AK3.  
DR MIM; 103030; -.  
DR InterPro: IPR000850; Adenylate\_kin.  
DR Pfam: PF00406; adenylatekinase; 1.  
DR PRINTS; PR00094; ADENYTKINASE.  
DR PRODOM; PD000657; Adenylate\_kin; 1.  
DR PROSITE; PS00113; ADENYLATE\_KINASE; 1.  
KW Transferase; Kinase; GTP-binding; Mitochondrion.  
FT NP\_BIND 12 GTP (BY SIMILARITY).  
SQ SEQUENCE 223 AA; 25268 MW; 653341A8EB3BC723 CRC64;  
Query Match 60.3%; Score 700.5; DB 1; Length 223;  
Best Local Similarity 58.8%; Pred. No. 2.3e-53;  
Matches 130; Conservative 38; Mismatches 52; Indels 1; Gaps 1;  
OY 4 SARLRVINGAPGSGKGYSSRTTTFELKHLSSGDLRLNMLRGTEIGVLAFAFDIG 63  
DB 2 ASKLLRAVILGPPGSGGTVCORIAONQLOHLSGHLRIRIKASTVEGMAKOYIEKS 61  
OY 64 KLIPDDVWTRLALHELKNTLYSWLDGFPRTLPOAALDRAVOIDTYININVPFEVTK 123  
DB 62 LLYVDHVTITRLMSELELRKQHWLIDGFPRTLPOAALDRAVLDVYSINIPETIKD 121  
OY 124 RLTAIRWHPASGRVYNIENFPKPTVGIDLTGEPLIQREDKPETVIKRLAYEDQTKV 183  
DB 122 RLRSRWHPSPGSRVYNDENFPHVIGIDVGEPLVQOEDDKPEVAARLQYDVAPV 181  
OY 184 LXYOKKGVLETFSGTEKNKIWPYVYAFLOTKV-PORSOKA 223  
DB 182 IELYKSRGVLIHQFSGTETNKIMPYVYLLFSNKRITPQSKEA 222  
RESULT 8  
KAD\_HAEIN STANDARD; PRT; 214 AA.  
AC P24323;  
DT 01-MAR-1992 (Rel. 21, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).  
GN AK4 OR H10349.  
OS Homo sapiens (Human).  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=RM 7004 / Serotype B;  
RA MEDLINE=92065797; PubMed=1956282;  
RA Maskell D.J., Szabo M.J., Butler P.D., Williams A.E., Moxon E.R.;  
RT "Molecular analysis of a complex locus from Haemophilus influenzae  
RL involved in phase-variable lipopolysaccharide biosynthesis.";  
RN Mol. Microbiol. 5:1013-1022(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Rd / KW20 / ATCC 51907;  
RX MEDLINE=9530630; PubMed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Knelavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McEweney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
RA Fine L.D., Fritchman J.L., Fritchman J.L., Geoghagen N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
RL Rd.";  
RN Science 269:496-512(1995).  
CC -1- FUNCTION: THIS SMALL UBQUITOUS ENZYME IS ESSENTIAL FOR  
CC MAINTENANCE AND CELL GROWTH. IT MAY BE LINKED TO THE BIOSYNTHESIS  
CC OF LIPOPOLYSACCHARIDE SURFACE MOLECULES, WHICH ARE IMPORTANT FOR  
CC THE PATHOGENESIS OF H. INFLUENZAE.  
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.  
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
CC -----  
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CC -----  
DR EMBL; X57315; CAA40570.1; -.  
DR EMBL; U32719; AAC22010.1; -.  
DR PIR; S15290; S15290.  
DR HSP; P05082; IE4Y.  
DR TIGR; H10349; -.  
DR InterPro: IPR000850; Adenylate\_kin.  
DR Pfam: PF00406; adenylatekinase; 1.  
DR PRINTS; PR00094; ADENYTKINASE.  
DR PRODOM; PD000657; Adenylate\_kin; 1.  
DR PROSITE; PS00113; ADENYLATE\_KINASE; 1.  
KW Transferase; Kinase; ATP-binding; Complete proteome.  
FT NP\_BIND 7 78 T -> A (IN REF. 1).  
FT CONFLICT 78 78 T -> A (IN REF. 1).  
SQ SEQUENCE 214 AA; 23508 MW; B83B630E93E1AAFC CRC64;  
Query Match 38.5%; Score 447.5; DB 1; Length 214;  
Best Local Similarity 46.1%; Pred. No. 1.3e-31;  
Matches 95; Conservative 37; Mismatches 61; Indels 13; Gaps 4;  
OY 8 LRAVIMGAPGSGKGYSSRTTTFELKHLSSGDLRLNMLRGTEIGVLAFAFDIGKILP 67  
DB 1 KRIILGAPGAGKQAOAIFNNKRGIPQISTGDMFAIRKAGTEIGKAKALMDGKILP 60  
OY 68 DD-----VWTRLALHELKNTLYSWLDGFPRTLPOAAL-DRAVOIDTYININVPFEVI 121



Db 181 YXQAEKAGNTKXFRLDGTRKV 202

RESULT 11  
KAD2\_YEAST

ID KAD2\_YEAST STANDARD: PRT: 225 AA.

AC P26364;  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 15-JUL-1992 (Rel. 36, Last annotation update)  
DE Adenylate kinase 2 (EC 2.7.4.3) (ATP-AMP transphosphorylase).  
GN ADK2 OR PAK3 OR YER170W.  
OS Saccharomyces cerevisiae (Baker's Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxId=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-92267376; PubMed-1587477;  
RA Cooper A.J., Friedberg E.C.;  
RT "A putative second adenylate kinase-encoding gene from the yeast  
Saccharomyces cerevisiae."  
RL Gene 114:145-148(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-92318888; PubMed-1620094;  
RA Schickler R., Magdolen V., Bandlow W.;  
RT "A new member of the adenylate kinase family in yeast: PAK3 is highly  
homologous to mammalian AK3 and is targeted to mitochondria."  
RL Mol. Gen. Genet. 233:363-371(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX STRAIN-DL-1;  
RA Dieckrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,  
RA Aviles E., Berro A., Brennan T., Carpenter J., Chen E., Cherry J.M.,  
RA Chung E., Duncan M., Guman E., Hartzell G., Hunnicke-Smith S.,  
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,  
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oelner P., Oh C.,  
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,  
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;  
RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR  
MAINTENANCE AND CELL GROWTH.  
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.  
CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.

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CC -----

DR EMBL: M77757; AAA34418.1; -  
DR EMBL: X65126; CAA46254.1; -  
DR EMBL: U18922; AAB64697.1; -  
DR PIR: J01135; J01135.  
DR PIR: S23568; S23568.  
DR HSSP: P08760; ZAK3.  
DR SGD: S0000972; ADK2.  
DR InterPro: IPR000850; Adenylate\_kin.  
DR Pfam: PF00406; adenylatekinase\_1.  
DR PRINTS: PR00094; ADENYLTKINASE.  
DR ProDom: PD000657; Adenylate\_kinase\_1.  
DR PROSITE: PS00113; ADENYLATE\_KINASE\_1.  
KW Transferase; kinase; ATP-binding; Mitochondrion.  
FT NP\_BIND 21 29 ATP (by SIMILARITY).  
SQ SEQUENCE 225 AA; 25194 MW; 3B192BE2535BF91F CRC64;

Query Match 37.9%; Score 439.5; DB 1; Length 225;  
Best local Similarity 44.9%; Pred. No. 7e-31;  
Matches 93; Conservative 37; Mismatches 66; Indels 11; Gaps 4;

QY 8 LRAVINGAPSGKGVSSRTTHF-ELKHLSSGDLRLDNMLRGTETGVLAKEAFIDGKLT 66  
DB 15 LRLLLGAPSGKGTOTSRLLKQIPOLSSISSGDIILROEIKSESTLGGREATVYIAQKLT 74  
QY 67 PDDVMTRLALHEKLN-----TOYSWLLDGPRLPQAEALDRAYQ-----IDVINLNP 117  
DB 75 PDDLRLTLTLFRISALGWLKPSAMWLDGPRTTAQSALDELKQHDASLNLVELDVP 134  
QY 118 FEVTKORLFRWHPASGRVYNIENFPKPTGVIGIDDLGEPDIOREDKPEYIKRLKAYE 177  
DB 135 ESTILIERIENRYHVPSGRVYNQYNPPKYPGLDDITGEPLTRRDDPAEVFKRLREYK 194  
QY 178 DQPKXVLYXYYQKKVLETSGETETNKI 204  
DB 195 KTNELPKDYKKSGIFGVSG-ETSDI 220

RESULT 12  
KAD\_ARATH

ID KAD\_ARATH STANDARD: PRT: 246 AA.

AC 082514; 09FPMW2;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).  
GN ADK1 OR ATSG63400 OR MLE2.3.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxId=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN-cv. Columbia;  
RA Weerts B., Thurnburg R.;  
RT "Characterization of the cDNA and gene for the Arabidopsis thaliana  
adenylate kinase."  
RL (in) Plant Gene Register PGR98-166.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN-cv. Columbia;  
RA MEDLINE-98162728; PubMed-9501997;  
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,  
RA Tabata S.;

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CC -----

DR EMBL: AF082882; AAC78478.1; -  
DR EMBL: AB007649; BAB08805.1; -  
DR HSSP: P07170; IAKY.  
DR InterPro: IPR000850; Adenylate\_kin.  
DR Pfam: PF00406; adenylatekinase\_1.  
DR PRINTS: PR00094; ADENYLTKINASE.  
DR ProDom: PD000657; Adenylate\_kinase\_1.  
DR PROSITE: PS00113; ADENYLATE\_KINASE\_1.





RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Ogell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skellon J., Simmonds N., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,  
 RA Welfens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Medler H., Wambolt R., Purnelle B.,  
 RA Galbault A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,  
 RA Gaillet F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of *Schizosaccharomyces pombe*.";  
 RL Nature 415:871-880(2002).  
 CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR  
 CC MAINTENANCE AND CELL GROWTH.  
 CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.  
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X70363; CAA49826.1; -;  
 DR EMBL: Z69727; CAA93553.1; -;  
 DR PIR: S31338; S31338.  
 DR PIR: A46718; A46718.  
 DR HSSP: P07170; IAKY.  
 DR InterPro: IPR000850; Adenylate\_kin.  
 DR Pfam: PF00406; adenylatekinase; 1.  
 DR PRINTS: PR00094; ADENYLTKINASE.  
 DR ProDom: PD000657; Adenylate\_kin; 1.  
 DR ProSite: PS00113; ADENYLATE\_KINASE; 1.  
 DR K: Kinase; ATP-binding.  
 FT NP\_BIND 10 18 ATP (BY SIMILARITY).  
 SQ SEQUENCE 220 AA; 24375 MW; F5335A025C971D78 CRC64;  
 Query Match 37.6%; Score 436; DB 1; Length 220;  
 Best Local Similarity 40.7%; Pred. No. 1.4e-30;  
 Matches 87; Conservative 46; Mismatches 73; Indels 8; Gaps 3;  
 YQ 8 LRAVINGAPSGSGTYSRTTHFELKHTSSGDLRDMKRGFIYGLARFIIDGKLIP 67  
 DB 4 MRLILVGPAGGTQAPNIOKKRYGIAHLADMLRQVARELGEAKRIMDGGGLVS 63  
 YQ 68 DVMATRLALHELKNTQ--YSMLDGFPRILPOAEAL-----DRAYQIDYVININVEFEV 120  
 DB 64 DDLVTGMIKEILINPECKKGFILDFPRTRYVQAERKLTALLDELKLDLNTVLELQVDEL 123  
 YQ 121 IKORLRAWIHPASGRVYNIEFPKPTVGIDLTGEPLLIGREDDKPEVTYLRKAYEDQT 180  
 DB 124 LVRIRIGRLVHPGSGRSYHLEFNPVKPMKDVTGGEPLLIORDNDALRKRRLTYHEQT 183  
 YQ 181 KXVLXYOKKGVLETSGET-TKKIWPYVYAFQ 213  
 DB 184 TPVVEFKKKGMAVDAACKPEQWQIVALE 217

DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Adenylate kinase cytosolic (EC 2.7.4.3) (ATP-AMP transphosphorylase).  
 GN AK1 OR AK1 OR AK1 OR AK2 OR YDR226W OR YD9934.11.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID:4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-88194690; PubMed-2834097;  
 RA Magdoen V., Oechsner U., Bandlow W.;  
 RT "The complete nucleotide sequence of the gene coding for yeast  
 RT adenylate kinase.";  
 RL Curr. Genet. 12:405-411(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-88015563; PubMed-2821496;  
 RA Proba K., Tomaselli A.G., Nielsen P., Schulz G.E.;  
 RT "The cdna sequence encoding cytosolic adenylate kinase from baker's  
 RT yeast (*Saccharomyces cerevisiae*).";  
 RL Nucleic Acids Res. 15:7187-7187(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-89066766; PubMed-2848829;  
 RA Konrad M.;  
 RT "Analysis and in vivo disruption of the gene coding for adenylate  
 RT kinase (ADK1) in the yeast *Saccharomyces cerevisiae*.";  
 RL J. Biol. Chem. 263:19468-19474(1988).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95192063; PubMed-7885847;  
 RA Davies C.J., Hutchison C.A. III;  
 RT "Insertion site specificity of the transposon Tn3.";  
 RL Nucleic Acids Res. 23:507-514(1995).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S288c / AB972;  
 RA Murphy L., Harris D.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE OF 3-222.  
 RX MEDLINE-86136113; PubMed-3004985;  
 RA Tomaselli A.G., Mast E., Jones W., Schlitz E.;  
 RT "The complete amino acid sequence of adenylate kinase from baker's  
 RT yeast.";  
 RL Eur. J. Biochem. 155:111-119(1986).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (1.63 ANGSTROMS).  
 RX MEDLINE-95400193; PubMed-7670369;  
 RA Abele U., Schulz G.E.;  
 RT "High-resolution structures of adenylate kinase from yeast ligated  
 RT with inhibitor Ap5a, showing the pathway of phosphoryl transfer.";  
 RL Protein Sci. 4:1262-1271(1995).  
 CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR  
 CC MAINTENANCE AND CELL GROWTH.  
 CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M18455; AAA6319.1; -;  
 DR EMBL: U13239; AAC33143.1; -;  
 DR EMBL: Y00413; CAA68471.1; -;  
 DR EMBL: X06304; CAA29624.1; -;



DR EMBL: Z48612; CAA88506.1; -.  
DR PIR: S05799; KIBIA.  
DR PIR: S47934; S47934.  
DR PIR: S47475; S47475.  
DR PDB: 1AKY; 14-NOV-95.  
DR PDB: 2AKY; 14-NOV-95.  
DR PDB: 3AKY; 14-NOV-95.  
DR PDB: 1DVR; 03-APR-96.  
DR SWISS-2DPAGE; P07170; YEAST.  
DR SGD: S0002634; ADK1.  
DR InterPro: IPR000850; Adenylate\_kin.  
DR pfam: PF00406; adenylatekinase; 1.  
DR PRINTS; PR00094; ADENYLKINASE.  
DR PRODOM; PD000657; Adenylate\_kin; 1.  
DR PROSITE; PS00113; ADENYLATE\_KINASE; 1.  
KW transferase; kinase; Acetylation; ATP-binding; 3D-structure.  
FT PROPEP 1 222 REMOVED IN MATURE FORM.  
FT CHAIN 3 222 ADENYLATE KINASE CYTOSOLIC.  
FT MOD\_RES 3 3 ACETYLTATION.  
FT NP\_BIND 13 21 ATP (BY SIMILARITY).  
FT CONFLICT 139 139 A -> R (IN REF. 2).  
FT CONFLICT 222 222 D -> N (IN REF. 6).  
SQ SEQUENCE 222 AA; 24255 MW; FE566FD8015907CE CRC64;

Query Match 37.5%; Score 435; DB 1; Length 222;  
Best Local Similarity 40.3%; Pred. No. 1.7e-30;  
Matches 89; Conservative 50; Mismatches 72; Indels 10; Gaps 3;

OY 3 ASARLLRAVIMGAPSGSGKGVSSRITTHFELKHLSSGDLIRDMLGTEIGVLAFAFDQ 62  
DB 2 SSESIRWVLIGPPGAKGTQAPNLQERFHAHLATGDMLSQIAKGTOLGLEAKKIMDQ 61  
OY 63 GKLIPIDVNTRLALHELKN--LTQYSMLDGEFPTLPOAALDRAYQ----IDTVYNLN 115  
DB 62 GGLVSDIDIVNMKDELTNPNACKNGEILDGFPRTIPQAEKLDQMLKEGTPLEKAIELK 121  
OY 116 VPPEVTKQRLTAMTHIPASGRVYNIEFPNPKTVGIDDLTGEPLIQREDDKPTVTKRLKA 175  
DB 122 VDDELVARITGRILIH PASGRSYHKIFNPKEKMDKDDVTGEALVQSRSDNADALKRRLAA 181  
OY 176 YEDQTKXVLYYOKKGVLEFEGSTETNKIMPYVYAFIQTKV 216  
DB 182 YHAQTEPIYDFYTKGTI--WAGVDASOPPATWADILNKL 219

Search completed: March 19, 2003, 16:08:48  
Job time : 314 secs

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OM protein - protein search, using sw model

Run on: March 19, 2003, 15:45:51 ; Search time 272 seconds

(without alignments)  
24.555 Million cell updates/sec

Title: US-10-006-190-1

Perfect score: 1161

Sequence: 1 MGASARLLRAVIMGAPSGK.....VYAFIQTKVQRSSQKASVTP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/1aa/5C\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/1aa/5D\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1157	99.7	227	2	US-08-829-027-1
2	1157	99.7	227	3	US-09-225-366-1
3	1156	99.6	227	4	US-09-149-476-377
4	1091	94.0	227	2	US-08-829-027-3
5	1091	94.0	227	3	US-09-225-366-3
6	1038	89.4	227	2	US-08-829-027-4
7	1038	89.4	227	3	US-09-225-366-4
8	700.5	60.3	223	2	US-08-829-027-5
9	700.5	60.3	223	3	US-09-225-366-5
10	412.5	35.5	222	4	US-09-134-001C-3289
11	222.5	19.2	194	2	US-08-879-561-12
12	221	19.0	194	2	US-08-879-561-11
13	187	16.1	197	2	US-08-879-561-5
14	81	7.0	488	4	US-08-985-343-1
15	80.5	6.9	620	4	US-08-637-670-40
16	80.5	6.9	620	4	US-08-335-844A-24
17	78	6.7	373	4	US-09-071-035-116
18	78	6.7	406	4	US-09-071-035-114
19	76.5	6.6	531	4	US-08-687-590-29
20	76.5	6.6	284	4	US-09-134-001C-3329
21	76	6.5	1027	4	US-09-134-001C-4188
22	76	6.5	1027	4	US-09-162-021B-2
23	75.5	6.5	464	4	US-09-134-001C-4562
24	74.5	6.4	335	4	US-08-987-146-2
25	74.5	6.4	419	4	US-09-120-426-2
26	73.5	6.3	898	1	US-08-036-210-22
27	73.5	6.3	898	2	US-08-449-609-22

28	73	6.3	408	2	US-08-683-007A-2	Sequence 2, Appl1
29	73	6.3	600	4	US-09-134-001C-3636	Sequence 3636, Ap
30	72.5	6.2	296	1	US-08-241-465B-21	Sequence 21, Appl
31	72.5	6.2	491	3	US-08-923-454A-14	Sequence 14, Appl
32	72.5	6.2	820	1	US-08-166-717D-6	Sequence 6, Appl1
33	72	6.2	229	4	US-09-134-001C-4113	Sequence 4113, Ap
34	72	6.2	303	2	US-08-321-670-2	Sequence 2, Appl1
35	72	6.2	303	4	US-09-215-252-3	Sequence 3, Appl1
36	71.5	6.2	1653	2	US-08-793-126-1	Sequence 1, Appl1
37	71.5	6.2	1653	4	US-09-132-271-1	Sequence 22, Appl
38	71.5	6.2	1663	4	US-09-142-334-22	Sequence 23, Appl
39	71.5	6.2	2089	1	US-08-418-893D-23	Sequence 24, Appl
40	71.5	6.2	2089	1	US-08-418-893D-24	Sequence 21, Appl
41	70.5	6.1	408	1	US-07-951-715A-21	Sequence 21, Appl
42	70.5	6.1	408	2	US-08-459-448A-21	Sequence 21, Appl
43	70.5	6.1	408	3	US-08-459-595A-21	Sequence 21, Appl
44	70.5	6.1	408	3	US-08-459-504B-21	Sequence 21, Appl
45	70.5	6.1	408	3	US-08-459-444-21	Sequence 21, Appl

## ALIGNMENTS

RESULT 1  
US-08-829-027-1  
; Sequence 1, Application US/08829027  
; Patent No. 5856160  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/829,027  
; FILING DATE: Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0256 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: Consensus  
; CLONE: 2122022  
; US-08-829-027-1  
Query Match 99.7%; Score 1157; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 4.3e-129;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGASARLLRAVIMGAPGSGKTVSSRITTHPELKLHSSGDLRDNNLRGNEIGVLAKAFI 60  
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Db 61 DOGKLIPDDVMTRLALHELNLTQYSMLLDGFPRTLPOAEALDRAVOIDVTINLNVPEV 120  
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Db 121 IKORLTARMIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDDEKPEYIKRLKAYEDOT 180  
Qy 181 KXVLXYXOKKGVLETFSGTETNKIMPYVYAFLOTKVPORSOKASVTP 227  
Db 181 KXVLXYXOKKGVLETFSGTETNKIMPYVYAFLOTKVPORSOKASVTP 227

RESULT 2  
US-09-225-366-1

; Sequence 1, Application US/09225366  
; Patent No. 6001624  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/225,366  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/829,027  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: Pf-0256 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: Consensus  
; CLONE: 2122022  
; US-09-225-366-1

Query Match 99.7%; Score 1157; DB 3; Length 227;  
Best Local Similarity 100.0%; Pred. No. 4,3e-129;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGASARLLRAVIMGAPGSGKTVSSRITTHPELKLHSSGDLRDNNLRGNEIGVLAKAFI 60  
Db 1 MGASARLLRAVIMGAPGSGKTVSSRITTHPELKLHSSGDLRDNNLRGNEIGVLAKAFI 60

Qy 61 DOGKLIPDDVMTRLALHELNLTQYSMLLDGFPRTLPOAEALDRAVOIDVTINLNVPEV 120  
Db 61 DOGKLIPDDVMTRLALHELNLTQYSMLLDGFPRTLPOAEALDRAVOIDVTINLNVPEV 120  
Qy 121 IKORLTARMIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDDEKPEYIKRLKAYEDOT 180  
Db 121 IKORLTARMIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDDEKPEYIKRLKAYEDOT 180  
Qy 181 KXVLXYXOKKGVLETFSGTETNKIMPYVYAFLOTKVPORSOKASVTP 227  
Db 181 KXVLXYXOKKGVLETFSGTETNKIMPYVYAFLOTKVPORSOKASVTP 227

RESULT 3  
US-09-149-476-377

; Sequence 377, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002p1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; EARLIER FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
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; EARLIER APPLICATION NUMBER: 60/047,633  
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; EARLIER APPLICATION NUMBER: 60/047,617  
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; EARLIER APPLICATION NUMBER: 60/047,618  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
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; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,613  
; EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,582  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,596  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,612  
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EARLIER FILING DATE: 1997-04-11  
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EARLIER APPLICATION NUMBER: 60/043,671  
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EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,672  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,889  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,878  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,662  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,637  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,880  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,894  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,874  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,910

EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,590  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 99.6%; Score 1156; DB 4; Length 227;  
Best Local Similarity 99.1%; Pred. No. 5,7e-129;  
Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPGSGKTVSSRITTHFELKHLSSGDLRDMLRGTEIGVLAKEFI 60  
DB 1 MGASARLLRAVIMGAPGSGKTVSSRITTHFELKHLSSGDLRDMLRGTEIGVLAKEFI 60  
QY 61 DOGKLIIPDDVMTRLALHELKNTQYSWLIDGFPRTLPOAEALDRAYQIDTVINLVNPPREV 120  
DB 61 DOGKLIIPDDVMTRLALHELKNTQYSWLIDGFPRTLPOAEALDRAYQIDTVINLVNPPREV 120  
QY 121 IKQRLTARWIHPASGRVYNIENFPKTVGIDDLTGEPLIQREDDKPEYIKRLKAYEODT 180  
DB 121 IKQRLTARWIHPASGRVYNIENFPKTVGIDDLTGEPLIQREDDKPEYIKRLKAYEODT 180  
QY 181 KXVLAYQOKKGVLETFSGTETNKIMPYVYAFLOTKVPQSRKASYTP 227  
DB 181 KXVLAYQOKKGVLETFSGTETNKIMPYVYAFLOTKVPQSRKASYTP 227

RESULT 4  
US-08-829-027-3  
; Sequence 3, Application US/08829027  
; Patent No. 5856160  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/829,027  
; FILING DATE: Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0256 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: Genbank  
; CLONE: 217576  
US-08-829-027-3

Query Match 94.0%; Score 1091; DB 2; Length 227;  
Best Local Similarity 91.6%; Pred. No. 3e-121;  
Matches 208; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPGSGKTVSSRITTHFELKHLSSGDLRDMLRGTEIGVLAKEFI 60  
DB 1 MGASARLLRAVIMGAPGSGKTVSSRITTHFELKHLSSGDLRDMLRGTEIGVLAKEFI 60

QY 61 DOGKLIIPDDVMTRLALHELKNTQYSWLIDGFPRTLPOAEALDRAYQIDTVINLVNPPREV 120  
DB 61 DOGKLIIPDDVMTRLALHELKNTQYSWLIDGFPRTLPOAEALDRAYQIDTVINLVNPPREV 120  
QY 121 IKQRLTARWIHPASGRVYNIENFPKTVGIDDLTGEPLIQREDDKPEYIKRLKAYEODT 180  
DB 121 IKQRLTARWIHPASGRVYNIENFPKTVGIDDLTGEPLIQREDDKPEYIKRLKAYEODT 180  
QY 181 KXVLAYQOKKGVLETFSGTETNKIMPYVYAFLOTKVPQSRKASYTP 227  
DB 181 KXVLAYQOKKGVLETFSGTETNKIMPYVYAFLOTKVPQSRKASYTP 227

RESULT 5  
US-09-225-366-3  
; Sequence 3, Application US/09225366  
; Patent No. 6001624  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/225,366  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/829,027  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0256 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: Genbank  
; CLONE: 217576  
US-09-225-366-3

Query Match 94.0%; Score 1091; DB 3; Length 227;  
Best Local Similarity 91.6%; Pred. No. 3e-121;  
Matches 208; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPGSGKTVSSRITTHFELKHLSSGDLRDMLRGTEIGVLAKEFI 60  
DB 1 MGASARLLRAVIMGAPGSGKTVSSRITTHFELKHLSSGDLRDMLRGTEIGVLAKEFI 60  
QY 61 DOGKLIIPDDVMTRLALHELKNTQYSWLIDGFPRTLPOAEALDRAYQIDTVINLVNPPREV 120  
DB 61 DOGKLIIPDDVMTRLALHELKNTQYSWLIDGFPRTLPOAEALDRAYQIDTVINLVNPPREV 120  
QY 121 IKQRLTARWIHPASGRVYNIENFPKTVGIDDLTGEPLIQREDDKPEYIKRLKAYEODT 180

Db 121 IKORLTARWHPASGRVYNIENFNPCKTGMGIDDLTGEPLVQREDRPEVTYKRLKAYEAO 180

QY 181 KXVLYYQKKGVLETFSGTETNKIMPYVYAFLOTXVQORSOKASVTP 227  
Db 181 EPLYEYRKKGVLTFSGTETNKIMPHYVAFLOTKLPORSOETSIVTP 227

## RESULT 6

US-08-829-027-4  
Sequence 4, Application US/08829027  
Patent No. 5856160  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/829,027  
FILING DATE: Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0256 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 450312  
US-08-829-027-4

Query Match 89.4%; Score 1038; DB 2; Length 227;  
Best Local Similarity 90.3%; Pred. No. 5.8e-115;  
Matches 205; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGASARLLRAVINGAPSGKGTSSRTTTFELKHLSSGDLRDNMGRGTEIGVLAFAFI 60  
Db 1 MGASGRLLRAVINGAPSGKGTSSRTTKHFELKHLSSGDLRLQNMLOGTETIAVLAKSFI 60  
QY 61 DQKLLIPDDVMTRLALHELKNTQYSWLDGFFPTLPQAEALDRAVOIDTVINLNVPFEV 120  
Db 61 DQKLLIPDDMTRLALHELKNTQCSWLDGFFPTLPQAEALDRAVOIDTVINLNVPFEV 120  
QY 121 IKORLTARWHPASGRVYNIENFNPCKTVGIDDLTGEPLIQREDKPEVTYKRLKAYEDOT 180  
Db 121 IKRLTARWHPASGRVYNIENFNPCKTVGIDDLTGEPLIQREDKPEVTYKRLKAYEAO 180  
QY 181 KXVLYYQKKGVLETFSGTETNKIMPYVYAFLOTXVQORSOKASVTP 227  
Db 181 EPLYEYRKKGVLTFSGTETNKIRPHYVSFLQKKVPETIQKASVTP 227

Db 181 EPLYOYRKKGVLTFSGTETNKIRPHYVSFLQKKVPETIQKASVTP 227

RESULT 7  
US-09-225-366-4  
Sequence 4, Application US/09225366  
Patent No. 6001624

GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,366  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/829,027  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0256 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 450312  
US-09-225-366-4

Query Match 89.4%; Score 1038; DB 3; Length 227;  
Best Local Similarity 90.3%; Pred. No. 5.8e-115;  
Matches 205; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGASARLLRAVINGAPSGKGTSSRTTTFELKHLSSGDLRDNMGRGTEIGVLAFAFI 60  
Db 1 MGASGRLLRAVINGAPSGKGTSSRTTKHFELKHLSSGDLRLQNMLOGTETIAVLAKSFI 60  
QY 61 DQKLLIPDDVMTRLALHELKNTQYSWLDGFFPTLPQAEALDRAVOIDTVINLNVPFEV 120  
Db 61 DQKLLIPDDMTRLALHELKNTQCSWLDGFFPTLPQAEALDRAVOIDTVINLNVPFEV 120  
QY 121 IKORLTARWHPASGRVYNIENFNPCKTVGIDDLTGEPLIQREDKPEVTYKRLKAYEDOT 180  
Db 121 IKRLTARWHPASGRVYNIENFNPCKTVGIDDLTGEPLIQREDKPEVTYKRLKAYEAO 180  
QY 181 KXVLYYQKKGVLETFSGTETNKIMPYVYAFLOTXVQORSOKASVTP 227  
Db 181 EPLYOYRKKGVLTFSGTETNKIRPHYVSFLQKKVPETIQKASVTP 227  
RESULT 8  
US-08-829-027-5

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Sequence 5, Application US/08829027
Patent No. 5856160
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,027
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0256 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 28577
US-08-829-027-5

Query Match          60.3%; Score 700.5; DB 2; Length 223;
Best Local Similarity 58.8%; Pred. No. 6.4e-75;
Matches 130; Conservative 38; Mismatches 52; Indels 1; Gaps 1;
```

```
US-09-225-366-5
Sequence 5, Application US/09225366
Patent No. 6001624
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
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TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,366
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/829,027
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0256 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 28577
US-09-225-366-5

Query Match          60.3%; Score 700.5; DB 3; Length 223;
Best Local Similarity 58.8%; Pred. No. 6.4e-75;
Matches 130; Conservative 38; Mismatches 52; Indels 1; Gaps 1;
```

```
US-09-134-001C-3289
Sequence 3289, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1996-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
```



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; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3289
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3289

Query Match
Best Local Similarity 41.3%; Pred. No. 9.7e-41;
Matches 86; Conservative 41; Mismatches 70; Indels 11; Gaps 3;

QY 8 LKAVIMGAGSGKGTSSRTTTFELKHLSSGDLDRNMLRGTEIGVLAFAFDGKLPD 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 8 MIIILGLGAGGTQASIVKFKPIPHISTGDMFKRAIKDETDLKEKASYMDRELVP 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 68 DDMTRLALHEL-KNLQYSMLDGFPRTLPOEALDRAY-----QIDVYINLVPEEVI 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 DEVTGIVKVERISEDKAKGFLIDGFPRTIDQAESLNQIMSELDREIDAVINIEVEEEL 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 122 KQRLTRKWHLPASGRVNIENPNPKTVGIDDLTGEPLIOREDDKPETVIRLKAVEDQTK 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 128 MNRLTGRICERKCGTYTHLVFNPKVDGICDIDGKLYOREDDNPETVSNRLSVNKKQSK 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 XVLYXYOKKGVLETFSGTE----TNKI 204
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 188 PILEYNNKGVLEKNIDGSKDIDEVTNDV 215
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-08-879-561-12
; Sequence 12, Application US/08879561
; Patent No. 5817482
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/879,561
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0325 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
```

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-879-561-12

Query Match
Best Local Similarity 28.3%; Pred. No. 2.8e-18;
Matches 58; Conservative 44; Mismatches 72; Indels 31; Gaps 5;

QY 12 IMGAPSGKGTSSRTTTFELKHLSSGDLDRNMLRGTEIGVLAFAFDGKLPD 71
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 14 VVGCPSSGKGTQCEKIVHKGYTHLSTGDLRAEVSSGSRGKLAIMEKGLVPLD 73
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 TRLALHEL-KNLQYSMLDGFPRTLPOEALDRAYQIDF-VINLVNPEEVIKORTAR 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 74 LDMRLDMALAKDTSKGFLLDGTPREVKQGEFEKKIAPPTLLLYDAGKETVWKRLLK 133
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 WHPASGRVNIENPNPKTVGIDDLTGEPLIOREDDKPETVIRLKAVEDQTKXVLY 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 134 --GETSGRV-----DNEETIKRRLTYKATEPVIAFYK 166
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QY 189 KKGVLTFSGTE-NKIPIVYVAF 212
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DB 167 GRCIVROLNAEGTVDEVFOQVCYL 191
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RESULT 12
US-08-879-561-11
; Sequence 11, Application US/08879561
; Patent No. 5817482
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/879,561
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0325 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-879-561-11
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US-08-985-343-1
: RESULT 14
: Sequence 1, Application US/08985343
: Patent No. 6468782
: GENERAL INFORMATION:
: APPLICANT: Tunnacliffe, Alan G.
: APPLICANT: Welsh, David T.
: APPLICANT: Roser, Bruce J.
: APPLICANT: Dhaliwal, Kamaljit S.
: APPLICANT: Colaco, Kamal
: TITLE OF INVENTION: METHODS OF PRESERVING PROKARYOTIC CELLS
: TITLE OF INVENTION: AND COMPOSITIONS OBTAINED THEREBY
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 PAGE MILL ROAD
: CITY: PALO ALTO
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/985,343
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Lehnhardt, Susan K.
: REGISTRATION NUMBER: 33,943
: REFERENCE/DOCKET NUMBER: 26374-20017.00
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 813-5600
: TELEFAX: (650) 494-0792
: TELEX: 706141 MRSNFOERS SFO
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 488 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-08-985-343-1
:
: Query Match 7.0%; Score 81; DB 4; Length 488;
: Best Local Similarity 24.2%; Pred. No. 0.74;
: Matches 48; Conservative 20; Mismatches 60; Indels 70; Gaps 11;
:
: 65 LIPDDVMTRLALHEKNLTQYSWLL-DSFP-----RTLPQAE----- 100
: | | : | : : | | | |
: 161 LIPDKIRQIVAKTKNI-KIGMFLHPFPSSSEIYRIILPVROELIKGVLSODLIGFHTYD 219
:
: 101 -----ALDAAYIDIVYINLNVEFEVKRIETARWHPASGRVYNIEFNPPTVGIDDL 153

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Db      220 YARHFLSAVORILNVTLPN-GVEFD-----GRFVWGAFF---IGIDVE 260
QY      154 TGEPLIQREDDKPEYVYIKRKAYEDQTKV-----LXYT---QKGVLETFEGTET 201
Db      261 T-----FTGGLKODAVIKRKIKESFKCKIIIGVDRLDYIKGVPOKHLALEVFLGAHP 315
QY      202 NKIMPYVVAFLQTKVPOR 219
Db      316 E--WICKVVLQVAVPSR 331
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## RESULT 15

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US-08-637-670-40
; Sequence 40, Application US/08637670
; Patent No. 6413521
;
; GENERAL INFORMATION:
; APPLICANT: MCMICHAEL-PHILLIPS et al.
; TITLE OF INVENTION: Helminth Parasite Antigen with
; TITLE OF INVENTION: Aminopeptidase-like Activity
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barbara G. Ernst
; STREET: 555 13TH STREET, NW Suite 701E
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,670
; FILING DATE: 26-JUN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1811-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 620 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-637-670-40
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## Query Match

6.9%: Score 80.5; DB 4; Length 620;

Best Local Similarity 23.8%; Pred. No. 1.2; Mismatches 54; Indels 71; Gaps 11;

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Matches 46; Conservative 22;
QY      25 SRTTHPELKHLSGDL-----LRDNLRGTEIGVLAKAFIDQKLIIPDDVWTRL 74
Db      35 ARIVAH-ELAHQWFGDLVTKMKWDNLNMGFAFTE-----FIGAGQITQDDAMR- 85
QY      75 ALHELKLNLOYSWLLDGFPTTLPOAELDRAYIDTVINLNVPFEVIKORLTARWIHPAS 134
Db      86 -----NY-FLID-----VLERALKADSVAS-----SHPLS 109
QY      135 GRVYNIEFNPPTKVGIDDLTGEPILQREDDKPEYVYIKRLKAY--EDQTKXVLXYYQKGV 192
Db      110 ---FRIDKAAVEAEAFDDITYA-----KGSVLMLRALIGEEKHHAASQYLRK-- 156
QY      193 LETFSGTETNKIW 205
Db      157 -FSYSNAEATDLW 168
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Search completed: March 19, 2003, 16:49:22  
Job time : 277 secs

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GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 Comugen Ltd.

OM protein - protein search, using sw model

Run on: March 19, 2003, 13:33:14 ; Search time 1047 Seconds

(without alignments)  
28.890 Million cell updates/sec

Title: US-10-006-190-1

Perfect score: 1161  
Sequence: 1 MGASARLLRAVIMGAPGSGK.....VYAFIQTKVPQRSGKASVTP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A.Geneseq\_101002:\*  
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1157	99.7	227	19 AAW81101	Human mitochondria
2	1156	99.6	227	19 AAW74787	Human secreted pro
3	1156	99.6	227	22 AAM38899	Human polypeptide
4	1156	99.6	227	22 AAB92887	Human protein sequ
5	1156	99.6	227	22 AAB93066	Human protein sequ
6	1156	99.6	227	22 AAB93487	Human protein sequ
7	1156	99.6	227	22 AAB85885	Human adenylate ki
8	1156	99.6	239	22 ABB12326	Human secreted pro
9	1156	99.6	239	22 AAM40685	Human polypeptide
10	1156	99.6	22	22 AAG73865	Human colon cancer

11	1130	97.3	227	21 AAB12440	Human mitochondria
12	1091	94.0	227	21 AAB12441	AK3 protein sequen
13	1048	90.3	214	21 AAB53619	Human colon cancer
14	655	56.4	224	22 AAE11778	Human kinase (PKIN
15	639	55.0	335	22 ABB23968	Novel human diago
16	565	48.7	216	22 ABB62530	Drosophila melanog
17	522.5	45.0	159	22 AAG65046	Human mitochondria
18	455	39.2	116	22 AAU17302	Human signal trans
19	447.5	38.5	214	22 AAU35415	Haemophilus influe
20	446	38.4	229	21 AAG15752	Arabidopsis thaila
21	446	38.4	228	21 AAG15751	Arabidopsis thaila
22	446	38.4	248	21 AAG15750	Arabidopsis thaila
23	439	37.8	229	21 AAG47327	Arabidopsis thaila
24	439	37.8	238	21 AAG47325	Arabidopsis thaila
25	438	37.8	248	21 AAG47325	Arabidopsis thaila
26	438	37.7	228	21 AAG41910	Arabidopsis thaila
27	438	37.7	246	21 AAG41909	Arabidopsis thaila
28	431	37.1	232	20 AAU77257	Human adenylate ki
29	431	37.1	237	23 ABB41753	Human ovarian anti
30	424	36.5	215	22 AAU36349	Pseudomonas aerugi
31	421	36.3	224	22 AAU36634	Staphylococcus aur
32	421	36.3	224	22 AAU37231	Staphylococcus aur
33	419.5	36.1	238	22 ABB19263	Novel human diago
34	417	35.9	215	22 AAU34046	Staphylococcus aur
35	413	35.6	214	22 AAU38124	Salmoneilla typhi c
36	412.5	35.5	222	23 ABB38444	Staphylococcus epi
37	411.5	35.4	215	22 AAG82243	S. epidermidis ope
38	410	35.3	215	23 ABB48630	Listeria monocytog
39	409	35.2	214	22 AAU36040	Klebsiella pneumon
40	405	34.9	214	22 AAU34482	E. coli cellular p
41	394	33.9	238	22 ABB25695	Novel human diago
42	378	32.6	647	22 ABB59655	Drosophila melanog
43	374	32.2	212	22 AAU37526	Streptococcus pneu
44	369.5	31.8	213	22 AAU33593	Enterococcus faeca
45	369.5	31.8	22	22 AAU34943	Enterococcus faeca

#### ALIGNMENTS

RESULT 1	
AAW81101	
ID	AAW81101 standard; Protein; 227 AA.
AC	AAW81101;
DT	29-JAN-1999 (first entry)
XX	
DE	Human mitochondrial adenylate kinase protein.
XX	
KW	Human; mitochondrial; adenylate kinase; therapeutic;
KW	neurological disorder; Alzheimer; Huntington; epilepsy; cancer;
KW	neural; inflammation; immune.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Misc-difference 182
FT	Misc-difference 185
FT	Misc-difference 185
XX	
PN	WO9844124-A1.
XX	
PD	08-OCT-1998.
XX	
PF	30-MAR-1998; 98WO-US06249.
XX	
PR	31-MAR-1997; 97US-0829027.
XX	
PA	(INCY-) INCYTE PHARM INC.
XX	
PI	Hillman JL, Shah P;

XX WPI: 1998-557119/47.  
DR N-PSDB: AAV68223.  
XX  
XX Human mitochondrial adenylate kinase, HMAK - useful e.g. to treat  
PT neurological disorders such as Alzheimer's and screen for  
PT antagonists for treatment of cancer or immunological disorders  
XX  
XX Claim 5; Fig 1; 63pp; English.  
XX  
CC The human mitochondrial adenylate kinase (HMAK) protein of 227 amino  
CC acids ) can be administered therapeutically, especially by expressing  
CC encoding polypeptides, to treat neurological disorders e.g. Alzheimer's  
CC disease, Huntington's disease, epilepsy. It can be combined with a  
CC suitable carrier in pharmaceutical compositions, which can be  
CC administered to treat such disorders. HMAK was shown to have chemical  
CC and structural homology with adenylate kinase isozyme 3 (AK3) from cow,  
CC rat and human (92, 91 and 57 % identity respectively) and was expressed  
CC in e.g. cancerous tissues, brain and neural tissues and tissues involved  
CC in inflammation and the immune response. Increased activity or  
CC expression was proposed to be associated with cancer and immunological  
CC disorders, and decreased activity/expression with the development of  
CC neurological disorders. Products of the above invention may be used in  
CC the diagnosis and treatment of the above diseases and disorders.  
XX  
SQ Sequence 227 AA:  
  
Query Match 99.7%; Score 1157; DB 19; Length 227;  
Best Local Similarity 100.0%; Pred. No. 2.1e-111;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGASARLLRAVIMGAPGSGKTGVSRTITTFELKHLSSGDLRLDMLRSTETGVLAKAFI 60  
DB 1 MGASARLLRAVIMGAPGSGKTGVSRTITTFELKHLSSGDLRLDMLRSTETGVLAKAFI 60  
OY 61 DGGKLIIPDVMTRLALHEKNTQYSWLDGFPRLPQAEALDRAVOITFVNLNVPFV 120  
DB 61 DGGKLIIPDVMTRLALHEKNTQYSWLDGFPRLPQAEALDRAVOITFVNLNVPFV 120  
OY 121 IKQRLTARMIHPASGRVYIEFNPPKTVGIDDLTGEPILQREDDKPEYIKRLKAYEDDT 180  
DB 121 IKQRLTARMIHPASGRVYIEFNPPKTVGIDDLTGEPILQREDDKPEYIKRLKAYEDDT 180  
OY 181 KXVLXYQKKGVLETFSGETNKIMPYVYAFLOTQVPORSQKASYTP 227  
DB 181 KXVLXYQKKGVLETFSGETNKIMPYVYAFLOTQVPORSQKASYTP 227

RESULT 2  
AAW74787  
ID AAW74787 standard; Protein; 227 AA.  
AC AAW74787;  
XX  
DT 19-JAN-1999 (first entry)  
XX  
XX Human secreted protein encoded by gene 58 clone HHFHN61.  
DE  
XX  
KW Human; secreted protein; testis; tumour; foetal brain tissue;  
KW fusion protein; cancer; central nervous system; seizure;  
KW diagnosis; neurodegenerative disease.  
XX  
XX Homo sapiens.  
OS  
XX  
PN MO9839448-A2.  
PD 11-SEP-1998.  
XX  
XX 06-MAR-1998; 98WO-US04493.  
PF  
XX 02-OCT-1997; 97US-0061060.  
PR 07-MAR-1997; 97US-0038621.  
PR 07-MAR-1997; 97US-0040161.  
PR

PR 07-MAR-1997; 97US-0040162.  
PR 07-MAR-1997; 97US-0040163.  
PR 07-MAR-1997; 97US-0040333.  
PR 07-MAR-1997; 97US-0040334.  
PR 07-MAR-1997; 97US-0040336.  
PR 07-MAR-1997; 97US-0040626.  
PR 11-APR-1997; 97US-0043311.  
PR 11-APR-1997; 97US-0043312.  
PR 11-APR-1997; 97US-0043313.  
PR 11-APR-1997; 97US-0043568.  
PR 11-APR-1997; 97US-0043569.  
PR 11-APR-1997; 97US-0043576.  
PR 11-APR-1997; 97US-0043578.  
PR 11-APR-1997; 97US-0043580.  
PR 11-APR-1997; 97US-0043659.  
PR 11-APR-1997; 97US-0043670.  
PR 11-APR-1997; 97US-0043671.  
PR 11-APR-1997; 97US-0043672.  
PR 11-APR-1997; 97US-0043674.  
PR 23-MAY-1997; 97US-0047492.  
PR 23-MAY-1997; 97US-0047500.  
PR 23-MAY-1997; 97US-0047501.  
PR 23-MAY-1997; 97US-0047502.  
PR 23-MAY-1997; 97US-0047503.  
PR 23-MAY-1997; 97US-0047581.  
PR 23-MAY-1997; 97US-0047582.  
PR 23-MAY-1997; 97US-0047583.  
PR 23-MAY-1997; 97US-0047584.  
PR 23-MAY-1997; 97US-0047585.  
PR 23-MAY-1997; 97US-0047586.  
PR 23-MAY-1997; 97US-0047587.  
PR 23-MAY-1997; 97US-0047588.  
PR 23-MAY-1997; 97US-0047589.  
PR 23-MAY-1997; 97US-0047590.  
PR 23-MAY-1997; 97US-0047592.  
PR 23-MAY-1997; 97US-0047593.  
PR 23-MAY-1997; 97US-0047594.  
PR 23-MAY-1997; 97US-0047595.  
PR 23-MAY-1997; 97US-0047596.  
PR 23-MAY-1997; 97US-0047597.  
PR 23-MAY-1997; 97US-0047598.  
PR 23-MAY-1997; 97US-0047599.  
PR 23-MAY-1997; 97US-0047600.  
PR 23-MAY-1997; 97US-0047601.  
PR 23-MAY-1997; 97US-0047612.  
PR 23-MAY-1997; 97US-0047613.  
PR 23-MAY-1997; 97US-0047614.  
PR 23-MAY-1997; 97US-0047615.  
PR 23-MAY-1997; 97US-0047617.  
PR 23-MAY-1997; 97US-0047618.  
PR 23-MAY-1997; 97US-0047632.  
PR 23-MAY-1997; 97US-0047633.  
PR 06-JUN-1997; 97US-0048964.  
PR 06-JUN-1997; 97US-0048974.  
PR 13-JUN-1997; 97US-0049610.  
PR 08-JUL-1997; 97US-0051926.  
PR 16-JUL-1997; 97US-0052874.  
PR 18-AUG-1997; 97US-0053724.  
PR 22-AUG-1997; 97US-0056630.  
PR 22-AUG-1997; 97US-0056631.  
PR 22-AUG-1997; 97US-0056632.  
PR 22-AUG-1997; 97US-0056636.  
PR 22-AUG-1997; 97US-0056637.  
PR 22-AUG-1997; 97US-0056662.  
PR 22-AUG-1997; 97US-0056664.  
PR 22-AUG-1997; 97US-0056845.  
PR 22-AUG-1997; 97US-0056846.  
PR 22-AUG-1997; 97US-0056864.  
PR 22-AUG-1997; 97US-0056872.  
PR 22-AUG-1997; 97US-0056874.  
PR 22-AUG-1997; 97US-0056875.  
PR 22-AUG-1997; 97US-0056876.



Query Match 99.6%; Score 1156; DB 22; Length 227;  
 Best Local Similarity 99.1%; Pred. No. 2.7e-111;  
 Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPSGSGKGVSSRITTHFELKHLSSGDLRDMLRGTETGVLAKAFI 60  
 |||  
 DB 1 MASARLLRAVIMGAPSGSGKGVSSRITTHFELKHLSSGDLRDMLRGTETGVLAKAFI 60  
 |||

QY 61 DQGLIPDDVMTRLALHEKNTLTQYSWLDGFPRTLPOAEALDRAYQIDTVINLWPFV 120  
 |||  
 DB 61 DQGLIPDDVMTRLALHEKNTLTQYSWLDGFPRTLPOAEALDRAYQIDTVINLWPFV 120  
 |||

QY 121 IKQRLTARWIHPASGRVNIIEFNPKTVGIDDLTGEPILQREDDKPEYIKRLKAYEDOT 180  
 |||  
 DB 121 IKQRLTARWIHPASGRVNIIEFNPKTVGIDDLTGEPILQREDDKPEYIKRLKAYEDOT 180  
 |||

QY 181 KXVLXYQKKGVLETFSGTETNKIMPYVYAFLOTQVPORSQKASVTP 227  
 |||  
 DB 181 KXVLXYQKKGVLETFSGTETNKIMPYVYAFLOTQVPORSQKASVTP 227  
 |||

RESULT 4  
 AAB92887  
 ID AAB92887 standard; Protein; 227 AA.  
 AC AAB92887;  
 XX  
 DT 26-JUN-2001 (first entry)  
 XX  
 DE Human protein sequence SEQ ID NO:11492.  
 KM Human; primer: detection; diagnosis; antisense therapy; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 EV EPI074617-A2.  
 XX  
 PD 07-FEB-2001.  
 XX  
 PF 28-JUL-2000; 2000EP-0116126.  
 XX  
 PR 29-JUL-1999; 99JP-0248036.  
 PR 27-AUG-1999; 99JP-0300253.  
 PR 11-JAN-2000; 2000JP-0118776.  
 PR 02-MAY-2000; 2000JP-0183767.  
 PR 09-JUN-2000; 2000JP-0241899.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX  
 DR WPI; 2001-318749/34.  
 XX  
 PT Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -  
 XX  
 PS Claim 8; SEQ ID 11492; 2537bp + CD ROM; English.  
 XX  
 CC The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.

Sequence 227 AA:  
 SQ  
 Query Match 99.6%; Score 1156; DB 22; Length 227;  
 Best Local Similarity 99.1%; Pred. No. 2.7e-111;  
 Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPSGSGKGVSSRITTHFELKHLSSGDLRDMLRGTETGVLAKAFI 60  
 |||  
 DB 1 MGASARLLRAVIMGAPSGSGKGVSSRITTHFELKHLSSGDLRDMLRGTETGVLAKAFI 60  
 |||

QY 61 DQGLIPDDVMTRLALHEKNTLTQYSWLDGFPRTLPOAEALDRAYQIDTVINLWPFV 120  
 |||  
 DB 61 DQGLIPDDVMTRLALHEKNTLTQYSWLDGFPRTLPOAEALDRAYQIDTVINLWPFV 120  
 |||

QY 121 IKQRLTARWIHPASGRVNIIEFNPKTVGIDDLTGEPILQREDDKPEYIKRLKAYEDOT 180  
 |||  
 DB 121 IKQRLTARWIHPASGRVNIIEFNPKTVGIDDLTGEPILQREDDKPEYIKRLKAYEDOT 180  
 |||

QY 181 KXVLXYQKKGVLETFSGTETNKIMPYVYAFLOTQVPORSQKASVTP 227  
 |||  
 DB 181 KXVLXYQKKGVLETFSGTETNKIMPYVYAFLOTQVPORSQKASVTP 227  
 |||

RESULT 5  
 AAB93066  
 ID AAB93066 standard; Protein; 227 AA.  
 AC AAB93066;  
 XX  
 DT 26-JUN-2001 (first entry)  
 XX  
 DE Human protein sequence SEQ ID NO:11883.  
 KM Human; primer: detection; diagnosis; antisense therapy; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 EV EPI074617-A2.  
 XX  
 PD 07-FEB-2001.  
 XX  
 PF 28-JUL-2000; 2000EP-0116126.  
 XX  
 PR 29-JUL-1999; 99JP-0248036.  
 PR 27-AUG-1999; 99JP-0300253.  
 PR 11-JAN-2000; 2000JP-0118776.  
 PR 02-MAY-2000; 2000JP-0183767.  
 PR 09-JUN-2000; 2000JP-0241899.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX  
 DR WPI; 2001-318749/34.  
 XX  
 PT Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -  
 XX  
 PS Claim 8; SEQ ID 11883; 2537bp + CD ROM; English.



XX The present invention describes primer sets for synthesizing 5602  
CC full-length cDNAs defined in the specification. Where a primer set  
CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary  
CC to the complementary strand of a polynucleotide which comprises one of  
CC the 5602 nucleotide sequences defined in the specification, where the  
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
CC of an oligonucleotide comprising a sequence complementary to the  
CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a  
CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in  
CC the specification. The primer sets can be used in antisense therapy and  
CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
CC represent oligonucleotides, all of which are used in the exemplification  
CC of the present invention.

XX Sequence 227 AA:

Query Match 99.6%; Score 1156; DB 22; Length 227;  
Best Local Similarity 99.1%; Pred. No. 2.7e-111;  
Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MGASARLLRAVIMGAPSGSGKGVSSRTITTFELKHLSSGDLRLDNLRGTEIGVLAKAFI 60  
DB 1 MGASARLLRAVIMGAPSGSGKGVSSRTITTFELKHLSSGDLRLDNLRGTEIGVLAKAFI 60  
OY 61 DQGKLIIPDDVMTRALHEKLNLTQYSWLDGFPRTLPQAEALDRAYQIDTVINLVNPFVEY 120  
DB 61 DQGKLIIPDDVMTRALHEKLNLTQYSWLDGFPRTLPQAEALDRAYQIDTVINLVNPFVEY 120  
OY 121 IKORLTARMIHPASGRVYNIENFPKTVGIDLTGEPRLQREDDKPEYIKRLKAYEDQT 180  
DB 121 IKORLTARMIHPASGRVYNIENFPKTVGIDLTGEPRLQREDDKPEYIKRLKAYEDQT 180  
OY 181 KXVLYXQKKGVLTFSTETNKIMPYVYAFLOTQKVPQSKASVTP 227  
DB 181 KXVLYXQKKGVLTFSTETNKIMPYVYAFLOTQKVPQSKASVTP 227

RESULT 6

AAB93487 AAB93487 standard; Protein: 227 AA.

XX AAB93487;

XX 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO.12786.

KW Human; primer: detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

XX 02-MAY-2000; 2000JP-0183767.

XX 09-JUN-2000; 2000JP-0241899.

PA (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI: 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602  
PT full-length cDNAs defined in the specification, and for the detection  
PT and/or diagnosis of the abnormality of the proteins encoded by the  
PT full-length cDNAs -

XX Claim 8; SEQ ID 12786; 2537bp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602  
CC full-length cDNAs defined in the specification. Where a primer set  
CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary  
CC to the complementary strand of a polynucleotide which comprises one of  
CC the 5602 nucleotide sequences defined in the specification, where the  
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
CC of an oligonucleotide comprising a sequence complementary to the  
CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a  
CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in  
CC the specification. The primer sets can be used in antisense therapy and  
CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
CC represent oligonucleotides, all of which are used in the exemplification  
CC of the present invention.

XX Sequence 227 AA:

Query Match 99.6%; Score 1156; DB 22; Length 227;  
Best Local Similarity 99.1%; Pred. No. 2.7e-111;  
Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MGASARLLRAVIMGAPSGSGKGVSSRTITTFELKHLSSGDLRLDNLRGTEIGVLAKAFI 60  
DB 1 MGASARLLRAVIMGAPSGSGKGVSSRTITTFELKHLSSGDLRLDNLRGTEIGVLAKAFI 60  
OY 61 DQGKLIIPDDVMTRALHEKLNLTQYSWLDGFPRTLPQAEALDRAYQIDTVINLVNPFVEY 120  
DB 61 DQGKLIIPDDVMTRALHEKLNLTQYSWLDGFPRTLPQAEALDRAYQIDTVINLVNPFVEY 120  
OY 121 IKORLTARMIHPASGRVYNIENFPKTVGIDLTGEPRLQREDDKPEYIKRLKAYEDQT 180  
DB 121 IKORLTARMIHPASGRVYNIENFPKTVGIDLTGEPRLQREDDKPEYIKRLKAYEDQT 180  
OY 181 KXVLYXQKKGVLTFSTETNKIMPYVYAFLOTQKVPQSKASVTP 227  
DB 181 KXVLYXQKKGVLTFSTETNKIMPYVYAFLOTQKVPQSKASVTP 227

RESULT 7

AAB85885 AAB85885 standard; Protein: 227 AA.

XX AAB85885;

XX 30-NOV-2001 (first entry)

DE Human adenylate kinase 3 (AK3)-like protein.

XX Adenylate kinase 3-like protein; AK3-like protein; AK3; cell morphology;

XX MELAS; central nervous system disorder; epilepsy; skeletal muscle;

KW muscle disease; electron transfer disorder; Leber disease; human;

KW diabetes mellitus; Peason disease; Parkinson's disease.  
 OS Homo sapiens.  
 XX WO200109346-A1.  
 XX 08-FEB-2001.  
 XX 28-JUL-2000; 2000WO-JP05066.  
 XX 29-JUL-1999; 99JP-0248036.  
 PR 27-AUG-1999; 99JP-0300253.  
 PR 18-OCT-1999; 99US-0159590.  
 PR 11-JAN-2000; 2000JP-0118776.  
 PR 17-FEB-2000; 2000US-0183322.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Isogai T, Hayashi K, Saito K, Yamamoto J, Ishii S;  
 PI Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Ihara S, Nakae H;  
 PI Nishikawa T, Kimura K;  
 XX  
 DR MPI: 2001-564737/63.  
 DR N-PSDB; AAA47197.  
 XX  
 PT New gene encoding an adenylyate kinase 3-like protein, and the protein  
 PT and antibodies to it, useful for diagnosis of brain disease e.g.  
 PT epilepsy, muscle disease, genetic disorder, diabetes -  
 XX  
 PS Claim 1; Page 34-35; 41pp; Japanese.  
 XX  
 CC The invention relates to a cDNA (clone C-NT2RP2000329) encoding a novel  
 CC adenylyate kinase 3 (AK3)-like protein. C-NT2RP2000329 has functions of  
 CC converting extracellular signals into intracellular signals and changing  
 CC cell morphology. The AK3-like protein, polynucleotides and antibodies are  
 CC useful in the investigation of diseases such as MELAS (cerebral accident  
 CC condition with hyperlacticacidemia), central nervous system disorder,  
 CC epilepsy, skeletal muscle conditions, muscle disease, electron transfer  
 CC disorders, Leber disease, diabetes mellitus, Peason disease, Parkinson's  
 CC disease, metabolism disorders. They are useful for developing diagnostics  
 CC and treatment agents. The present sequence represents the human AK3-like  
 CC protein of the invention.  
 CC  
 XX  
 SQ Sequence 227 AA;  
 Query Match 99.6%; Score 1156; DB 22; Length 227;  
 Best Local Similarity 99.1%; Pred. No. 2,7e-111;  
 Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query 1 MGASARLLRAVIMGAPSGSGKTSSRTTHFELKHLSSGDLRLDMLRGTEIGVLAKAFI 60  
 DB 1 MGASARLLRAVIMGAPSGSGKTSSRTTHFELKHLSSGDLRLDMLRGTEIGVLAKAFI 60  
 QY 61 DOGKLIIPDWMTRALHLEKMLTQYSWLLDGFPRRLPOAEALDRAKYQIDTYINLWPREV 120  
 DB 61 DOGKLIIPDWMTRALHLEKMLTQYSWLLDGFPRRLPOAEALDRAKYQIDTYINLWPREV 120  
 QY 121 IKORLTAMWIPASGRVNIENFPKTYGIDLTGEPIQREDDPEYIKRLKAYEDOT 180  
 DB 121 IKORLTAMWIPASGRVNIENFPKTYGIDLTGEPIQREDDPEYIKRLKAYEDOT 180  
 QY 181 KXVLXYOKKGVLETFSGTETNKKIMPVYVAFLOQTKVPORSOKASVTP 227  
 DB 181 KPVLEYOKKGVLETFSGTETNKKIMPVYVAFLOQTKVPORSOKASVTP 227

RESULT 8  
 ABB12326  
 ID ABB12326 standard; peptide: 239 AA.  
 XX  
 AC ABB12326;  
 XX  
 DT 11-JAN-2002 (first entry)

XX  
 DE Human secreted protein homologue, SEQ ID NO:2696.  
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;  
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; antiinflammatory;  
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW cytosstatic; osteopapic; vasotropic; cardiant; virucide; antibacterial;  
 KW antifungal; vulnerary; antulcer.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200157188-A2.  
 XX  
 XX 09-AUG-2001.  
 XX  
 XX 05-FEB-2001; 2001WO-US03800.  
 XX  
 XX 03-FEB-2000; 2000US-0496914.  
 PR 27-APR-2000; 2000US-0560875.  
 XX  
 XX (HXSE-) HXSEQ INC.  
 PA  
 XX  
 PI Tang YF, Liu C, Drmanac RT;  
 PI MPI: 2001-457740/49.  
 DR N-PSDB; ABA09570.  
 XX  
 PT Human proteins and DNA encoding sequences useful for preventing,  
 PT treating or ameliorating a medical condition in a mammalian subject  
 PT e.g. arthritis and cancer -  
 XX  
 PS Claim 20; Page 333; 1963pp; English.  
 XX  
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities, stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a novel human  
 CC polypeptide of the invention.

XX SQ Sequence 239 AA;

Query Match 99.6%; Score 1156; DB 22; Length 239;  
 Best Local Similarity 99.1%; Pred. No. 2,9e-111;  
 Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPSGKGVSSRIITTFELKHLSSGDLRDNMRLRGTEIGVLAFAFI 60  
 DB 13 MGASARLLRAVIMGAPSGKGVSSRIITTFELKHLSSGDLRDNMRLRGTEIGVLAFAFI 72  
 QY 61 DQGLIPDDVMTRLALHELKLNLTQYSWLDGFPRTLPQAEALDRAYQIDTVINLNVPEV 120  
 DB 73 DQGLIPDDVMTRLALHELKLNLTQYSWLDGFPRTLPQAEALDRAYQIDTVINLNVPEV 132  
 QY 121 IKQRLTARWTHIPASGRVNIIEFNPRTKTVGIDDLTGEPILIOREDDKPTVIKRLKAYEDQT 180  
 DB 133 IKQRLTARWTHIPASGRVNIIEFNPRTKTVGIDDLTGEPILIOREDDKPTVIKRLKAYEDQT 192  
 QY 181 KXVLXYQKKGVLETFSGTETNKIMPYVYAFLOTKVPORSOKASVTP 227  
 DB 193 KXVLXYQKKGVLETFSGTETNKIMPYVYAFLOTKVPORSOKASVTP 239

RESULT 9  
 AAM40685

ID AAM40685 standard; Protein; 239 AA.

XX AC AAM40685;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 5616.

XX KW Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.

XX OS Homo sapiens.

XX PN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US34263.

XX PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX DR WPI: 2001-442253/47.  
 DR N-PSDB: AA159841.

PT Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -  
 XX  
 XX Example 2; SEQ ID NO 5616; 10078bp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AAM38642-AA442213) with noctropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.

XX SQ Sequence 239 AA;

Query Match 99.6%; Score 1156; DB 22; Length 239;  
 Best Local Similarity 99.1%; Pred. No. 2,9e-111;  
 Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPSGKGVSSRIITTFELKHLSSGDLRDNMRLRGTEIGVLAFAFI 60  
 DB 13 MGASARLLRAVIMGAPSGKGVSSRIITTFELKHLSSGDLRDNMRLRGTEIGVLAFAFI 72  
 QY 61 DQGLIPDDVMTRLALHELKLNLTQYSWLDGFPRTLPQAEALDRAYQIDTVINLNVPEV 120  
 DB 73 DQGLIPDDVMTRLALHELKLNLTQYSWLDGFPRTLPQAEALDRAYQIDTVINLNVPEV 132  
 QY 121 IKQRLTARWTHIPASGRVNIIEFNPRTKTVGIDDLTGEPILIOREDDKPTVIKRLKAYEDQT 180  
 DB 133 IKQRLTARWTHIPASGRVNIIEFNPRTKTVGIDDLTGEPILIOREDDKPTVIKRLKAYEDQT 192  
 QY 181 KXVLXYQKKGVLETFSGTETNKIMPYVYAFLOTKVPORSOKASVTP 227  
 DB 193 KXVLXYQKKGVLETFSGTETNKIMPYVYAFLOTKVPORSOKASVTP 239

RESULT 10

AAG73865

ID AAG73865 standard; Protein; 256 AA.

XX AC AAG73865;

XX DT 03-SEP-2001 (first entry)

XX DE Human colon cancer antigen protein SEQ ID NO:4629.

XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KW colorectal carcinoma.

XX OS Homo sapiens.

XX PN WO200122920-A2.

XX PD 05-APR-2001.

XX PF 28-SEP-2000; 2000WO-US26524.

XX PR 29-SEP-1999; 99US-0157137.  
 PR 03-NOV-1999; 99US-0163280.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;

XX DR WPI: 2001-235357/24.

DR N-PSDB; AAH3296.  
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
PT useful for preventing, diagnosing and/or treating colorectal cancers -  
XX  
XX  
PS Claim 11: Page 6430-6431; 9803pp; English.  
XX  
XX AAH32963 to AAH37195 and AAC73514 to AAC77788 represent human colon  
CC cancer-associated nucleic acid molecules (N) and proteins (P), where  
CC the proteins are collectively known as colon cancer antigens. The colon  
CC cancer antigens have cytostatic activity and can be used in gene  
CC therapy and vaccine production. N and P may be used in the prevention,  
CC diagnosis and treatment of diseases associated with inappropriate P  
CC expression. For example, N and P may be used to treat disorders  
CC associated with decreased expression by rectifying mutations or deletions  
CC in a patient's genome that affect the activity of P by expressing  
CC inactive proteins or to supplement the patient's own production of P.  
CC Additionally, N may be used to produce the colon cancer-associated Ps,  
CC by inserting the nucleic acids into a host cell and culturing the cell  
CC to express the proteins. N and P can be used in the prevention, diagnosis  
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204  
CC and AAC77789 represent sequences used in the exemplification of the  
CC present invention.  
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
CC missing at time of publication, meaning no sequences are present for  
CC SEQ ID NO:1027 to 1052, 7921 and 7922.  
XX

Sequence 256 AA:

Query Match 99.6%; Score 1156; DB 22; Length 256;  
Best Local Similarity 99.1%; Pred. No. 3.2e-111;  
Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGSARLRAVIMGAPSGKGVSSRTTHFEKLHSSGDLRDNNLRGTEIGVLAKAFI 60  
DB 30 MGSARLRAVIMGAPSGKGVSSRTTHFEKLHSSGDLRDNNLRGTEIGVLAKAFI 89  
QY 61 DQGLIPDDVMTRLALHEKLNLTQYSMLDGFPRTLPOAEALDRAYQIDTVINLVNPFVEY 120  
DB 90 DQGLIPDDVMTRLALHEKLNLTQYSMLDGFPRTLPOAEALDRAYQIDTVINLVNPFVEY 149  
QY 121 IKORLTARMIHPASGRVNIIEFNPKTVGIDDLTGEPRLIOREDKPEYIKRLKAYEDOT 180  
DB 150 IKORLTARMIHPASGRVNIIEFNPKTVGIDDLTGEPRLIOREDKPEYIKRLKAYEDOT 209  
QY 181 KXVLYYQKKGVLETFSGTETNKIMPYVAFLOTKVPOKRSOKASVTP 227  
DB 210 KXVLYYQKKGVLETFSGTETNKIMPYVAFLOTKVPOKRSOKASVTP 256

RESULT 11

AAH32963 standard; Protein: 227 AA.

AAH32963;

20-OCT-2000 (first entry)

Human mitochondrial GTP:AMP phosphotransferase SEQ ID NO:4.

Human; mitochondrial GTP:AMP phosphotransferase; GTP3P; ribotide.

Homo sapiens.

CN1249340-A.

05-APR-2000.

28-SEP-1998; 98CN-0119439.

28-SEP-1998; 98CN-0119439.

(XINH-) XINHUNGPU FUDAN GENE ENG CO LTD SHANGHA.

XX Yu L, Zhao Y, Bi A;  
PI WPI; 2000-400718/35.  
XX N-PSDB; AAA60582.  
DR Preparation of human mitochondrial matrix GTP : AMP phosphotransferase,  
PT its encode sequence -  
XX  
XX  
PS Claim 4: Page 14-15; 20pp; Chinese.  
XX  
XX The present invention describes a new ribotide sequence of human gene,  
CC that is, the cDNA sequence of human mitochondrial matrix GTP:AMP  
CC phosphotransferase (GTP3P) and the encoded polypeptide. The present  
CC sequence represents human GTP3P.  
XX

Sequence 227 AA:

Query Match 97.3%; Score 1130; DB 21; Length 227;  
Best Local Similarity 97.4%; Pred. No. 1.3e-108;  
Matches 221; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGSARLRAVIMGAPSGKGVSSRTTHFEKLHSSGDLRDNNLRGTEIGVLAKAFI 60  
DB 1 MGSARLRAVIMGAPSGKGVSSRTTHFEKLHSSGDLRDNNLRGTEIGVLAKAFI 60  
QY 61 DQGLIPDDVMTRLALHEKLNLTQYSMLDGFPRTLPOAEALDRAYQIDTVINLVNPFVEY 120  
DB 61 DQGLIPDDVMTRLALHEKLNLTQYSMLDGFPRTLPOAEALDRAYQIDTVINLVNPFVEY 120  
QY 121 IKORLTARMIHPASGRVNIIEFNPKTVGIDDLTGEPRLIOREDKPEYIKRLKAYEDOT 180  
DB 121 IKORLTARMIHPASGRVNIIEFNPKTVGIDDLTGEPRLIOREDKPEYIKRLKAYEDOT 180  
QY 181 KXVLYYQKKGVLETFSGTETNKIMPYVAFLOTKVPOKRSOKASVTP 227  
DB 181 KXVLYYQKKGVLETFSGTETNKIMPYVAFLOTKVPOKRSOKASVTP 227

RESULT 12

AAH32963 standard; Protein: 227 AA.

AAH32963;

20-OCT-2000 (first entry)

AK3 protein sequence.

Human; mitochondrial GTP:AMP phosphotransferase; GTP3P; ribotide.

Unidentified.

CN1249340-A.

05-APR-2000.

28-SEP-1998; 98CN-0119439.

28-SEP-1998; 98CN-0119439.

(XINH-) XINHUNGPU FUDAN GENE ENG CO LTD SHANGHA.

Yu L, Zhao Y, Bi A;

WPI; 2000-400718/35.

N-PSDB; AAA60585.

Preparation of human mitochondrial matrix GTP : AMP phosphotransferase,  
PT its encode sequence -

Example 2; Fig 2; 20pp; Chinese.

CC The present invention describes a new ribotide sequence of human gene,  
CC that is, the cDNA sequence of human mitochondrial matrix GTP:AMP  
CC phosphotransferase (GTP3P) and the encoded polypeptide. The present  
CC sequence represents the AK3 protein sequence which is used in  
CC comparison with human GTP3P in the present invention.

CC Sequence 227 AA:

Query Match 94.0%; Score 1091; DB 21; Length 227;  
Best Local Similarity 91.6%; Pred. No. 1.5e-104;

Matches 208; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

CC 1 MGASARLRAVINGAPSGSGKGVSSRTITTFELKHLSSGDLRDMLRGTETIGVLAKEAFI 60

CC 1 MGASARLRAVINGAPSGSGKGVSSRTITTFELKHLSSGDLRDMLRGTETIGVLAKEAFI 60

CC 61 DQGLIPDDVMTFLALHELNLTQYSWLLDGFPRTLPOAEALDRAYQIDVTINLNPFEV 120

CC 61 DQGLIPDDVMTFLALHELNLTQYSWLLDGFPRTLPOAEALDRAYQIDVTINLNPFEV 120

CC 121 IKQRLARINIHPSGRVYNIENPPTKTVGIDLTGEPLOREDKPEYIKRLKAYEDQT 180

CC 121 IKQRLARINIHPSGRVYNIENPPTKTVGIDLTGEPLOREDKPEYIKRLKAYEDQT 180

CC 181 KAVLYTYOKKGVETFSGETNKIMPYVYAFLOTQKVPORSQKASVMP 227

CC 181 EPVLEYTKRKGVLETFSGETNKIMPYVYAFLOTQKVPORSQKASVMP 227

RESULT 13

AAB53619  
ID AAB53619 standard; Protein; 214 AA.

AC AAB53619;

DT 09-MAR-2001 (first entry)

DE Human colon cancer antigen protein sequence SEQ ID NO:1159.

CC Human; colon cancer; colon cancer antigen; diagnosis; detection;

CC Identification; cytostatic; cardioactive; neuroprotective; vulnereary;

CC immunomodulatory; muscular; gynaecological; gastrointestinal;

CC nephrotropic; antiinfective; antibacterial; gene therapy; wound;

CC neural disorder; immune system disorder; muscular disorder;

CC reproductive disorder; gastrointestinal disorder; renal disorder;

CC infectious disease; cardiovascular disorder.

CC Homo sapiens.

CC MO20005351-A1.

CC 21-SEP-2000.

CC 08-MAR-2000; 2000WO-US05883.

CC 12-MAR-1999; 99US-0124270.

CC (HUMA-) HUMAN GENOME SCI INC.

CC Rosen CA, Ruben SM;

CC MPI: 2000-587534/55.

CC N-PSDB: AAC98376.

CC Colon cancer associated gene sequences, referred to as colon cancer  
CC antigens, useful for the treatment, prevention, and diagnosis of colon  
CC disorders such as colon cancer -

CC Claim 11; Page 1741-1742; 2104pp; English.  
CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,  
CC called human colon cancer antigens, given in AAB53334 to AAB54006. The  
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;

CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,  
CC vulnerary, nephrotropic, antiinfective and antibacterial activities, and  
CC can be used in gene therapy. The colon cancer antigen polynucleotides,  
CC proteins and antibodies to the proteins are useful for the prevention,  
CC treatment and diagnosis of colon disorders, such as colon cancer. The  
CC polynucleotides may be used in diagnostics and research, such as for  
CC chromosome identification, and as hybridisation probes. The proteins  
CC may also be used to prevent diseases such as neural disorders, immune  
CC system disorders, muscular disorders, reproductive disorders,  
CC gastrointestinal disorders, wounds, renal disorders, infectious  
CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and  
CC AAB54007 represent sequences used in the exemplification of the present  
CC invention.

CC Sequence 214 AA:

Query Match 90.3%; Score 1048; DB 21; Length 214;  
Best Local Similarity 95.3%; Pred. No. 3.8e-100;

Matches 203; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CC 10 AVIMGAPSGSGKGVSSRTITTFELKHLSSGDLRDMLRGTETIGVLAKEAFIDQGLIPDD 69

CC 1 AVIMGAPSGSGKGVSSRTITTFELKHLSSGDLRDMLRGTETIGVLAKEAFIDQGLIPDD 60

CC 70 VMTFLALHELNLTQYSWLLDGFPRTLPOAEALDRAYQIDVTINLNPFEVIRKRLTARM 129

CC 61 VMTFLALHELNLTQYSWLLDGFPRTLPOAEALDRAYQIDVTINLNPFEVIRKRLTARM 120

CC 130 IHPASGRVYNIENPPTKTVGIDLTGEPLOREDKPEYIKRLKAYEDQTKXVLYYOK 189

CC 121 IHPASGRVYNIENPPTKTVGIDLTGEPLOREDKPEYIKRLKAYEDQTKXVLYYOK 180

CC 190 KGVLETFSGTETNKIMPYVYAFLOTQKVPORSQK 222

CC 181 KGVLETFSGTETNKIMPYVYAFLOTQKVPORSQK 213

RESULT 14

AAB51778  
ID AAB51778 standard; Protein; 224 AA.

AC AAB51778;

DT 18-DEC-2001 (first entry)

DE Human kinase (PKIN)-12 protein.

CC Human kinase; PKIN; gene therapy; adenocarcinoma; immune disorder; gout;

CC cancer; allergy; sarcoma; leukaemia; acquired immune deficiency syndrome;

CC AIDS; Addison's disease; microbial infection; inflammation; osteoporosis;

CC atherosclerosis; cardiovascular disease; myocardial infarction; anaemia;

CC myasthenia gravis; cirrhosis; cataract; growth and development disorder;

CC seizure disorder; pulmonary embolism; Gaucher's disease; lipid disorder;

CC lipid storage disease; Pick's disease; Tay-Sachs disease; renal disease;

CC obesity; restorative therapy; immunomodulatory; vaccine; cardiovascular;

CC antimicrobial; cytostatic; antiinflammatory; asthma.

CC Homo sapiens.

CC Key

CC Region

CC Region

CC Region

CC Region

CC Region

Location/Qualifiers

1..126

/note="Adenylate kinase"

8..23

/note="Shikimate kinase family"

9..25

/note="Adenylate kinase"

10..190

/note="Adenylate kinase"

33..76

/note="Adenylate kinase"

80..94

/note="Adenylate kinase"

85..96

/note="Adenylate kinase"

Domain

[illegible]

	QY	124	RILAFWHPASGRYYNIIEFNPKTGVIGIDLTGEPFLIOREDKDEKYIKLAKAYEDQTXYV	183
	Dd	122	RLSRWRHPPSGRYNYNLDNFNNPHVGJIDVTGEPLVOOEEDKEPEAAVRLLROYKVAPRV	181
	OY	164	LXYYOKRGVL--ETFSGTETNKIMPYVV-AFLQRKKVPQRSOKA	223
	Dd	182	IELYKSRCGLVHQFFRNRRTKMYPVYTTELKNITPIQSKEA	223
		RESULT_15		
	ID	ABG23968		
	XX	AC	ABG23968 standard; Protein; 335 AA.	
	XX	DT	18-FEB-2002 (first entry)	
	XX	DE	Novel human diagnostic protein #23959.	
	KM	Homo sapiens		
	OS	Homo sapiens		
	PD	WO200175067-A2.		
	XX	PD	11-OCT-2001.	
	PF	30-MAR-2001; 2001WO-USO08631.		
	PR	31-MAR-2000; 2000US-0540217.		
	PR	23-AUG-2000; 2000US-0649167.		
	PA	(HYSE-) HYSEQ INC.		
	XZ	Dymanac RT, Liu C, Tang YT,		
	DR	N-PADB; AAS88155.		
	PT	New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -		
	PS	Claim 20; SEQ ID No 54327; 103pp; English.		
	CC	The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. CC		
	CC	The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG3037 represent novel human diagnostic amino acid sequences of the invention. Note:		
	CC	Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.		
	S0	Sequence	335 AA;	
	Query Match	55.0%; Score 639;	DB 22;	Length 335;
	Best Local Similarity	54.9e%;	Pred No. 1.5e-57;	

Matches 123; Conservative 34; Mismatches 65; Indels 2; Gaps 2;

```

QY 4 SARLRAVIMGAPSGKGT-VSSRITTHFELKHLSSGDLRDNMKGTETIGVLAK-AFID 61
    : : ||||| : || || | : : ||||| || : || : :
Db 80 ASKLLRAVILGPPGLGAPVCORIAONFGLQHLSSGHFLRENIKASTEVEGEMAKOYRE 139
    : : ||||| : || || | : : ||||| || : || : :
QY 62 QGKLIPDDVWTRIALHELNLTQYSWLLDGFPTLPQAEALDRAYQIDTVINLNVPEVI 121
    : : ||||| : || || | : : ||||| || : || : :
Db 140 KYFLVDPDHVITRLMSELEENRGQHLLDGFPTFGQAEALDKICEVDVIRLNTISFETL 199
    : : ||||| : || || | : : ||||| || : || : :
QY 122 KORLTARWIHPASGRVYNIEFNPPTVIGIDLGEPLIQREDDKPTVIKRLKAYEDQTK 181
    : : ||||| : || || | : : ||||| || : || : :
Db 200 KDGILNRRIWHPSPGRVYNLDNFNPVHYGIDVTGEPLVQOEDDKPEAVAAARLRQYKDVAK 259
    : : ||||| : || || | : : ||||| || : || : :
QY 182 XVLXYYQKKGVLETFSGTETNKIWPYVYAFLOTRKVPQRSOKASY 225
    : : ||||| : || || | : : ||||| || : || : :
Db 260 PVLELYKSRGVLHQFSQETETNKIWPYVYTLFSNKRITPIQSKESI 303
    : : ||||| : || || | : : ||||| || : || : :

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Search completed: March 19, 2003, 16:03:22  
 Job time : 1049 secs

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GenCore version 5.1.4.p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 19:59:24 ; Search time 31295 Seconds

(without alignments)  
794.178 Million cell updates/sec

Title: US-10-006-190-2

Perfect score: 854

Sequence: 1 GCCAGCCCAAGCCCTGCT.....TGAATATATATTACTTTTA 854

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sy:\*

12: gb\_un:\*

13: gb\_vl:\*

14: em\_ba:\*

15: em\_fun:\*

16: em\_hum:\*

17: em\_mu:\*

18: em\_or:\*

19: em\_ov:\*

20: em\_pat:\*

21: em\_ph:\*

22: em\_pl:\*

23: em\_pr:\*

24: em\_ro:\*

25: em\_sy:\*

26: em\_un:\*

27: em\_vl:\*

28: em\_ba:\*

29: em\_fun:\*

30: em\_hum:\*

31: em\_mu:\*

32: em\_or:\*

33: em\_ov:\*

34: em\_pat:\*

35: em\_ph:\*

36: em\_pl:\*

37: em\_pr:\*

38: em\_ro:\*

39: em\_sy:\*

40: em\_un:\*

41: em\_vl:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	851	99.6	854	6	AR027227	AR027227 Sequence
2	851	99.6	854	6	AR094188	AR094188 Sequence
3	835.2	97.8	1667	9	BC013771	BC013771 Homo sapi
4	835.2	97.8	1701	9	AK001951	AK001951 Homo sapi
5	835.2	97.8	2642	9	AK001553	AK001553 Homo sapi
6	816	95.6	2394	6	BD012403	BD012403 Novel gen
7	816	95.6	2394	6	AK027534	AK027534 Homo sapi
8	816	95.6	2394	23	BD005083	BD005083 Novel gen
9	667.6	78.2	684	9	AB021870	AB021870 Homo sapi
10	653	76.5	1539	9	AF183419	AF183419 Homo sapi
11	653	76.5	3008	9	AK098205	AK098205 Homo sapi
12	613.6	71.9	3631	4	BOVPKIMP	M25757 Bovine mito
13	573.6	67.2	725	4	AF417508	AF417508 Oryctolab
14	573.4	67.1	1850	10	BC016432	BC016432 Mus muscu
15	573.4	67.1	1850	10	BC019174	BC019174 Mus muscu
16	573.4	67.1	2776	10	BC024871	BC024871 Mus muscu
17	572.4	67.0	77496	2	AC116082	AC116082 Rattus no
18	559.2	65.5	1061	10	RATKINASE3	D13062 Rat mRNA fo
19	542	63.5	973	10	AB020203	AB020203 Mus muscu
20	520.4	60.9	142080	2	AC069260	AC069260 Homo sapi
21	520.4	60.9	190283	2	AC067779	AC067779 Homo sapi
22	520.4	60.9	201821	2	AC129105	AC129105 Homo sapi
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24	518.8	60.7	148643	2	AC011871	AC011871 Homo sapi
25	518.8	60.7	154233	2	AC108701	AC108701 Homo sapi
26	518.8	60.7	183203	2	AC078930	AC078930 Homo sapi
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28	465.2	54.5	153792	2	AC094097	AC094097 Homo sapi
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31	463.6	54.3	210378	2	AL590967	AL590967 Homo sapi
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34	337.8	39.6	209669	2	AC091949	AC091949 Homo sapi
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36	332.2	38.9	208660	2	AC020577	AC020577 Homo sapi
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38	301.2	35.3	133475	2	AC006254	AC006254 Homo sapi
39	299.6	35.1	174613	2	AC019252	AC019252 Homo sapi
40	258.4	30.3	162959	2	AC019255	AC019255 Homo sapi
41	258.4	30.3	168292	2	AC068774	AC068774 Homo sapi
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44	255.2	29.9	69631	2	AC126386	AC126386 Homo sapi
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## ALIGNMENTS

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DEFINITION Sequence 2 from patent US 5856160.  
ACCESSION AR027227  
VERSION AR027227.1 GI:5938067  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 854)  
AUTHORS Hillman,J.L. and Shah,P.  
TITLE Mitochondrial adenylate kinase  
JOURNAL Patent: US 5856160-A 2 05-JAN-1999;  
FEATURES Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

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Best Local Similarity 100.0%; Pred. No. 3e-201;
Matches 854; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCCAGGCCCAAGGCCCTGTACCCCGGGGTGGGGCTTCAGTCTCGGCGCATGGGGCGGT 60
QY 61 CCGCGCGGCTGCTGGAGCGGTGATCATAGGGGGCCCCGGGCTCGGGCAAGGGCACCGTGT 120
DB 61 CCGCGCGGCTGCTGGAGCGGTGATCATAGGGGGCCCCGGGCTCGGGCAAGGGCACCGTGT 120
QY 121 CGTCGCGCATCTACACACTTCGAGCTGAAAGCACCTCTCCAGCGGGACCTGTCGGG 180
DB 121 CGTCGCGCATCTACACACTTCGAGCTGAAAGCACCTCTCCAGCGGGACCTGTCGGG 180
QY 181 ACAACATGCTGGGGGACAGAAATTTGGGTGAGCCAGGCTTTCATTGACCAAGGA 240
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QY 241 AACTCATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
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QY 481 CTCCCAAACTGTGGGCTGTGATGACTGATGGGGAGCTCTCTATTGAGCTGAGGATG 540
DB 481 CTCCCAAACTGTGGGCTGTGATGACTGATGGGGAGCTCTCTATTGAGCTGAGGATG 540
QY 541 ATAAACAGAGACGGTTATCAAGAGACTAAAGGCTTATGAAGACCAACAAAGNAGTCC 600
DB 541 ATAAACAGAGACGGTTATCAAGAGACTAAAGGCTTATGAAGACCAACAAAGNAGTCC 600
QY 601 TGGNATATTACAGAAAAAAGGGGTGCTGGAACATTTCTCCGGAACAGAAACCAAGGA 660
DB 601 TGGNATATTACAGAAAAAAGGGGTGCTGGAACATTTCTCCGGAACAGAAACCAAGGA 660
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DB 661 TTTGGCCCTATGATATATGCTTTCCACAACTAAAGTTCACAAAGAAAGCCGAAGGCTT 720
QY 721 CAGTTACTCATGAGAGAAATGTGTGTAAGTATTAATAGTAAGTGGGCAAACTCCTTA 780
DB 721 CAGTTACTCATGAGAGAAATGTGTGTAAGTATTAATAGTAAGTGGGCAAACTCCTTA 780
QY 781 GTCCCTGATTTAAGAGTGTCTTTCCTAAGACTTCTAGTATGATGAATCTTTGAAAA 840
DB 781 GTCCCTGATTTAAGAGTGTCTTTCCTAAGACTTCTAGTATGATGAATCTTTGAAAA 840
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DB 841 TTATATTACTTTTA 854

RESULT 2
AR094188
LOCUS AR094188 854 bp DNA linear PAT 08-SEP-2000
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DEFINITION Sequence 2 from patent US 6001624.
ACCESSION AR094188
VERSION AR094188.1 GI:10020933
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 854)
AUTHORS Hillman, J. L. and Shah, P.
TITLE Mitochondrial adenylate kinase
JOURNAL Patent: US 6001624-A 2 14-DEC-1999;
FEATURES
source 1. .854
/organism="unknown"
BASE COUNT 230 a 213 c 211 g 197 t 3 others
ORIGIN
Query Match 99.6%; Score 851; DB 6; Length 854;
Best Local Similarity 100.0%; Pred. No. 3e-201;
Matches 854; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CCGCGCGGCTGCTGGAGCGGTGATCATAGGGGGCCCCGGGCTCGGGCAAGGGCACCGTGT 120
DB 61 CCGCGCGGCTGCTGGAGCGGTGATCATAGGGGGCCCCGGGCTCGGGCAAGGGCACCGTGT 120
QY 121 CGTCGCGCATCTACACACTTCGAGCTGAAAGCACCTCTCCAGCGGGACCTGTCGGG 180
DB 121 CGTCGCGCATCTACACACTTCGAGCTGAAAGCACCTCTCCAGCGGGACCTGTCGGG 180
QY 181 ACAACATGCTGGGGGACAGAAATTTGGGTGAGCCAGGCTTTCATTGACCAAGGA 240
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DB 361 GAGCTTATCAGATCGACACAGTATGATTAACCTGAATGTCCTTTAGAGTCATTAAACA 420
QY 421 GCCTTACTGCTGCTGGATTATCCCGCCAGTGGCCAGTCTATTAACATTGAATTCACC 480
DB 421 GCCTTACTGCTGCTGGATTATCCCGCCAGTGGCCAGTCTATTAACATTGAATTCACC 480
QY 481 CTCCCAAACTGTGGGCTGTGATGACTGATGGGGAGCTCTCTATTGAGCTGAGGATG 540
DB 481 CTCCCAAACTGTGGGCTGTGATGACTGATGGGGAGCTCTCTATTGAGCTGAGGATG 540
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DB 541 ATAAACAGAGACGGTTATCAAGAGACTAAAGGCTTATGAAGACCAACAAAGNAGTCC 600
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DB 601 TGGNATATTACAGAAAAAAGGGGTGCTGGAACATTTCTCCGGAACAGAAACCAAGGA 660
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DB 661 TTTGGCCCTATGATATATGCTTTCCACAACTAAAGTTCACAAAGAAAGCCGAAGGCTT 720
QY 721 CAGTTACTCATGAGAGAAATGTGTGTAAGTATTAATAGTAAGTGGGCAAACTCCTTA 780
DB 721 CAGTTACTCATGAGAGAAATGTGTGTAAGTATTAATAGTAAGTGGGCAAACTCCTTA 780
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OY	781	GTCCTGCATTAAAGCTGCTTTTCCCAAGACCTCTAGTATGTGAATTCCTTGAAA	840
Db	781	GTCTTGCATTTAAGACTGCTTTTCCCAAGACCTCTAGTATGTGAATTCCTTGAAA	840
OY	841	TTATATACTTTTA	854
Db	841	TTATATACTTTTA	854
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DEFINITION	Homo sapiens, clone MGC:21124 IMAGE:4385034,	mRNA, complete cds.	
ACCESSION	BC013771		
VERSION	BC013771.1	GI:15489347	
KEYWORDS	MGC.		
SOURCE	Homo sapiens.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1667)		
TITLE	Strausberg, R.		
JOURNAL	Direct Submissions Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgaps-remail.nih.gov Tissue Procurement: Lou Straub cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: vllalad@bcm.tmc.edu, Villalon, D.K., Luna, R.A., Kale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.		
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Series: IRAC plate: 26 Row: O Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7023533. location/Qualifiers		
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Best Local Similarity	99.2%;	Pred. No. 2.8e-197;	
Matches 848; Conservative	0; Mismatches 6;	Indels 1;	Gaps 1;

OY	1	GCGNAGCCAAAGGCGCTGGTACCGCGCGGGTG-6GGCCTCAAGTCGTGGGCCATGGGGGCG	59
Db	6	GGCGAGGCGCAAAGCGCTGGTACC GGCGGGGCGGCGCTCAAGTCGTGGGCCATGGGGGCG	65
OY	60	TCCCGCGGCGTGTCTGCAGAGCGGTATCATTTGGGGGGCCCCGGGCGTGGGGCAAGGGCACCGTG	119
Db	66	TCGCGCGGCGTGTCTGCAGAGCGGTATCATTTGGGGGGCCCCGGGCGTGGGGCAAGGGCACCGTG	125
OY	120	TCGTGCGGCATCTACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGG	179
Db	126	TCGTGCGGCATCTACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGG	185
OY	180	GACAACATGCTGCGGGGGGACAGAATTGGCGTGTTAGCCAAGGCTTTATTGACCAAGG	239
Db	186	GACAACATGCTGCGGGGGGACAGAATTGGCGTGTTAGCCAAGGCTTTATTGACCAAGG	245
OY	240	AACACTATCCCAAGATGATGTCATGACTCGGCGGCGCTTCATGAGCTGAAAAATCTCAC	299
Db	246	AACACTATCCCAAGATGATGTCATGACTCGGCGGCGCTTCATGAGCTGAAAAATCTCAC	305
OY	300	CAGTATAGCTGGCGTGGTGATGTTTTCCAAGSACACTTCACACAGCAGAACGCCCTAGAT	359
Db	306	CAGTATAGCTGGCGTGGTGATGTTTTCCAAGSACACTTCACACAGCAGAACGCCCTAGAT	365
OY	360	AGAGCTATTCAGATCGACACAGTGTATACTGAATGTGCCCTTTGAGGTCTATTAACAA	419
Db	366	AGAGCTATTCAGATCGACACAGTGTATACTGAATGTGCCCTTTGAGGTCTATTAACAA	425
OY	420	CGCCTTACTGCTGGGTGATTCATCCGCGCAGTGGCGCAGTCTAATACATTGAATTCAAC	479
Db	426	CGCCTTACTGCTGGGTGATTCATCCGCGCAGTGGCGCAGTCTAATACATTGAATTCAAC	485
OY	480	CCCTCCCAAAACCTGTGGGCGATTGATGACCTGACTGGGAGCGCTCTCATTCACGCTGAGAT	539
Db	486	CCCTCCCAAAACCTGTGGGCGATTGATGACCTGACTGGGAGCGCTCTCATTCACGCTGAGAT	545
OY	540	GATTAACACGAGAGCGTTATCAAGAGACTAAAGCTTATGAAGACCAACAAAGNCAGTC	599
Db	546	GATTAACACGAGAGCGTTATCAAGAGACTAAAGCTTATGAAGACCAACAAAGNCAGTC	605
OY	600	CTGGATATTTCACGAAAAGGGGTGTGGAAACATCTCCGGAAACGAAACCAACAG	659
Db	606	CTGGATATTTCACGAAAAGGGGTGTGGAAACATCTCCGGAAACGAAACCAACAG	665
OY	660	ATTGGGCCCTATGATATATGCTTTCCTACAAACTAAAGTTCACAAAGAACGACAGAACT	719
Db	666	ATTGGGCCCTATGATATATGCTTTCCTACAAACTAAAGTTCACAAAGAACGACAGAACT	725
OY	720	TCAGTTACTCATGAGAGGAAATGTGTAACTATTAATAGTAGAGTGGCAACCTCT	779
Db	726	TCAGTTACTCATGAGAGGAAATGTGTAACTATTAATAGTAGAGTGGCAACCTCT	785
OY	780	AGTCTTTCGATTTAGAACCTGCTTTTCTTAGACTTTCAGTATGATGAATTTCTTGGAA	839
Db	786	AGTCTTTCGATTTAGAACCTGCTTTTCTTAGACTTTCAGTATGATGAATTTCTTGGAA	845
OY	840	ATTATATTACTTTTA	854
Db	846	ATTATATTACTTTTA	860
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DEFINITION		Homo sapiens cDNA FLJ11089 fis, clone PLACE1005305, highly similar	
ACCESSION		AK001951	
VERSION		AK001951.1 GI:7023533	
KEYWORDS		oligo cloning; flis (full insert sequence).	
SOURCE		Homo sapiens placenta cDNA to mRNA, clone_1lb.PLACE1	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1  
Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,  
Nishikawa,T., Nagai,K., Sugano,S., Aotsuka,S., Yoshikawa,Y.,  
Matsunawa,H., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,  
Wakamatsu,A., Nakamura,Y., Nagahara,I., Masuno,I. and Sasaki,N.  
NEO human cDNA sequencing project  
Unpublished  
2 (bases 1 to 1701)  
Isogai,T. and Otsuki,T.  
Direct Submission  
Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,  
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
(E-mail:genomcs@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
NEO human cDNA sequencing project supported by Ministry of  
International Trade and Industry of Japan: cDNA full insert  
sequencing: Research Association for Biotechnology: cDNA library  
construction, 5'- & 3'-end one pass sequencing and clone selection:  
Helix Research Institute (supported by Japan Key Technology Center  
etc.) and Department of Virology, Institute of Medical Science,  
University of Tokyo.

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Query Match 97.8%; Score 835.2; DB 9; Length 1701;  
Best Local Similarity 99.2%; Pred. No. 2.8e-197;  
Matches 848; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

1 GCCAGGCCCAAGACCCCTGTACCCGCGCGGTG-GGGCTCAGCTGCGGCCATGGGGCGG 59  
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3 TCCGCGCGCGCTCTCGAGCGGTGATCATGGGGCCCCGGGCTCGGGCAAGGGCAACCGTG 119  
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780 ACTCTTGCATTTAGAGAGCTGCTTTCTTCAAGACTTCTAGATTAATTAATTAATTAAT 839  
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RESULT 5  
AK001553  
LOCUS  
DEFINITION  
ACCESION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AK001553 2642 bp mRNA linear PRI 01-AUG-2002  
Homo sapiens cDNA FLJ10691 f1s, clone NT2RP3000359, highly similar  
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AK001553  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1  
Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,  
Nishikawa,T., Nagai,K., Sugano,S., Ishibashi,T., Fujimori,K.,  
Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Ishii,S., Kawai,Y.,  
Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahara,I.,  
Masuno,Y. and Kanehori,K.  
NEO human cDNA sequencing project  
Unpublished  
2 (bases 1 to 2642)  
Isogai,T. and Otsuki,T.  
Direct Submission  
Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,  
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
(E-mail:genomcs@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
NEO human cDNA sequencing project supported by Ministry of  
International Trade and Industry of Japan: cDNA full insert  
sequencing: Research Association for Biotechnology: cDNA library  
construction, 5'- & 3'-end one pass sequencing and clone selection:  
Helix Research Institute (supported by Japan Key Technology Center  
etc.) and Department of Virology, Institute of Medical Science,  
University of Tokyo.

FEATURES  
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LOCUS BD012403 2394 bp DNA linear PAT 02-AUG-2002
DEFINITION Novel genes encoding adenylate kinase 3(AK3) like proteins.
ACCESSION BD012403
VERSION BD012403.1 GI:22092592
KEYWORDS WO 0109346-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 2394)
AUTHORS Ota,T., Isogai,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S.,
Nishikawa,T., Makatsuta,A., Nagai,K., Otsuk,T., Ihara,S., Nake,H.,
Nishikawa,T., and Kimura,K.
Novel genes encoding adenylate kinase 3(AK3) like proteins
Patent: WO 0109346-A 1 08-FEB-2001;
HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,KOJI HAYASHI, AORU
SAITO, JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI
WAKAMATSU, KEIICHI NAGAI,TERUSUI OTSUKI,SHIGEO IHARA,HIROKI NAKAE,
ETSUO NISHIKAWA, KOICHI KIMURA
OS Homo sapiens (human)
PN WO 0109346-A/1
PD 08-FEB-2001
PE 28-JUL-2000 WO 2000JP005066
PR 29-JUL-1999 JP 99P 248036.27-AUG-1999 JP 99P 300253 PR
11-JAN-2000 JP 00P 118776.18-OCT-1999 US 66/159590 PR
17-FEB-2000 US 60/183322
PI TOSHIO OTA,TAKAO ISOGAI,KOJI HAYASHI,KAOBU SAITO, PI JUNICHI
YAMAMOTO,
PI SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,KEIICHI NAGAI, PI
TERUSUI OTSUKI,
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Best Local Similarity 99.8%; Pred. No. 1,8e-192;
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to GFP:AMP PHOSPHORANSEFERASE MITOCHONDRIAL (BC 2.7.4.10).  
ACCESSION AK027534  
VERSION AK027534.1 GI:14042280  
KEYWORDS oligo capping; fls (full insert sequence).  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1  
Iisogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,  
Nishikawa,T., Nagai,K., Sugano,S., Shiratori,H., Sudo,H.,  
Matsushima,M., Hosokiri,T., Kaku,Y., Kodaira,H., Kondo,H.,  
Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,  
Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,  
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,  
Nakamura,Y., Nagahara,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.  
NEO human cDNA sequencing project  
Unpublished  
JOURNAL 2 (bases 1 to 2394)  
REFERENCE Iisogai,T. and Otsuki,T.  
AUTHORS Direct Submission  
TITLE

JOURNAL Submitted (10-MAY-2001) Takao Iisogai, Helix Research Institute,  
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
COMMENT NEO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing;  
Research Association for Biotechnology; cDNA library construction;  
5'-6' and one pass sequencing and clone selection; Helix  
Research Institute (supported by Japan Key Technology Center etc.)  
and Department of Virology, Institute of Medical Science,  
University of Tokyo.

FEATURES  
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BASE COUNT 760 a 428 c 477 g 729 t  
ORIGIN

Query Match 95.6%; Score 816; DB 9; Length 2394;  
Best Local Similarity 99.8%; Pred. No. 1.8e-192;  
Matches 816; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 37 CTCAGCTTGGCGCCATTTGGGGGCGTCCGGGCTGCTCGAGAGGCTGATGATGGGGGCC 96  
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BD005083	
ID BD005083	standard; DNA; HUM; 2394 BP.

DT	08-FEB-2002 (Rel. 70, Created)
DT	08-FEB-2002 (Rel. 70, Last updated, Version 1)

Novel genes encoding adenylate kinase 3 (AK3) like proteins.

KW JP 03074939-T/1.

**Homo sapiens (human)**

OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.

[1]

RA Ota T., Isogai K., Hayashi K., Saito K., Yamamoto J., Ishii S.,

RA Nishikawa T., KIMURA K.i.  
RA Sugiyama I., Wakamatsu A., Nagai K., Otsuk T., Inaba S., Nakae H.

RI Novel genes encoding adenylate kinase 3 (AK3) like proteins";

KL HELIX RESEARCH INSTITUTE. .  
XX  
XX

CC	OS	Homo sapiens (human)
CC	PN	TP_03074939-T/1

CC	PD	30-JAN-2001	TP 2000005056
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CC	PR	29-JUL-1999	JP 99P	248036,27-AUG-1999	JP 99P	300253
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CC 17-FEB-2000 US 60/183322

CC JUNICHI YAMAMOTO,  
PI

CC PI TETSUJI OTSUKI,

CC	C12N15/54, C12N9/12, C12N1/21, C12P21/02, C07K16/40, C12Q1/68,
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				Gaps 0:

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Db

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Oy 217 CCAAGGCTTTCATGTGACCAAGGGAACATCATCCAGATGATGTATGACTCGGCTGGCC 276

Dh 181 CCAAGGCTTTCATGTGACCAAGGGAACATCATCCAGATGATGTATGACTCGGCTGGCC 240

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457 GAGCTCTATPACANTTGAATTCACCCCTCCCAAACGTGGGGCATTTGATGACCTGACTGGGG 516

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LOCUS	DEFINITION	AB021870
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AB021870		
LOCUS		
DEFINITION		
AB021870		
684 bp	mRNA	linear
Homo sapiens	hsk3alpha mRNA for adenylate kinase 3 alpha, complete	PRI 18-JAN-2002

CDs.  
AB021870

VERSION	AB021870.1	GI:6518532
KEYWORDS	NAK3alpha: adenylate kinase 3 alpha.	
SOURCE	Homo sapiens liver cDNA to mRNA.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 Noma,T., Fujisawa,K., Yamashiro,Y., Shinozawa,M., Nakazawa,A., Gondo,T., Ishihara,T. and Yoshinobu K.	
TITLE	Structure and expression of human mitochondrial adenylylate kinase targeted to the mitochondrial matrix	
JOURNAL	Biochem. J. 358 (Pt 1), 225-232 (2001)	
MEDLINE	21378190	
REFERENCE	2 (bases 1 to 684)	
AUTHORS	Noma,T.	
TITLE	Direct Submission	
JOURNAL	Submitted (25-DEC-1998) Takafumi Noma, Yamaguchi University School of Medicine, Department of Biochemistry, 1144 Kogushu, Ube, Yamaguchi 755-8505, Japan (E-mail: tlnoma@po.cc.yamaguchi-u.ac.jp, Tel:81-836-22-2215, Fax:81-836-22-2315)	
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FEATURES	source
LOCUS	AF183419
DEFINITION	AF183419 Homo sapiens GTP:AMP phosphotransferase mRNA, complete cds; nuclear gene for mitochondrial product.
ACCESSION	AF183419
VERSION	AF183419.1
KEYWORDS	GI:9963776
SOURCE	.
ORGANISM	Homo sapiens. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1. (bases 1 to 1539) 1. Y., Peng, Y., Jiang, Z., Gu, W., Han, Z. and Chen, Z. A novel gene expressed in human pheochromocytoma unpublished 2. (bases 1 to 1539) Peng, Y., Gu, W., Huang, C., Xu, S., Han, Z., Fu, G. and Chen, Z. Direct Submission Submitted (03-SEP-1999) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang HI-Tech Park, Pudong, Shanghai 201203, P. R. China Location/Qualifiers 1. 1539

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	BASE COUNT	514 a 273 c 282 g 470 t
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DEFINITION Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.									
ACCESSION M25757									
VERSION M25757.1 GI:163527									
KEYWORDS GTP:AMP phosphotransferase; adenylate kinase.									
SOURCE Bovine liver. cDNA to mRNA, clones									
lambda-bcaK3-[1-1.2-2.2-1.2-8.3-5.3-9.2-3.2-7].									
ORGANISM Bos taurus									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									



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DEFINITION Mus musculus, adenylate kinase 3 alpha like, clone MGC:255636
IMAGE:4217820, mRNA, complete cds.
ACCESSION BC016432
VERSION BC016432.1 GI:16741172
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
1 (bases 1 to 1850)
Strausberg, R.
Direct Submission
Submitted (31-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amegbcm.tmc.edu
Gunter, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

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Best Local Similarity 85.9% Pred. No. 4.8e-132;
Matches 634; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
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61 CCGCGCGCTGTGCGAGCGGTGATGAGGGGCGCGCGCTGCGGCAAGGCGCGTGT 120
86 CGGGGCGCGTGTGCGCGCGCTGTGATGAGGGGCGCGCGCTGCGGCAAGGCGCGTGT 145
121 CGTGGCGCATCTACACACTTTCAGAGTGAAGACACTTCTCAGGGGGAGCTGCTCGGG 180
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206 AGAACATGCTGCGAGGCGACAGAAATGCGTGTGTTGGCCAGACCTTTCATTGACCAAGGA 265
241 AACTCATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
266 AGCTGATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 325
301 AGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
326 AGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 385
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386 AAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 445
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DEFINITION Mus musculus, adenylate kinase 3 alpha like, clone MGC:29159
IMAGE:5007578, mRNA, complete cds.
ACCESSION BC019174
VERSION   BC019174.1 GI:17512427
KEYWORDS  MGC.
SOURCE    house mouse.
ORGANISM  Mus musculus.
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1860)
AUTHORS   Strausberg, R.
TITLE     Direct Submission
JOURNAL   Submitted (07-DEC-2001) National Institutes of Health, Mammalian
           Gene Collection (MGC), Cancer Genomics Office, National Cancer
           Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
           USA
REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
           Email: cgapbs@email.nih.gov
           Tissue Procurement: Gilbert Smith, Ph.D.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
           DNA Sequencing by: National Institutes of Health Intramural
           Sequencing Center (NISC),
           Gaithersburg, Maryland;
           Web site: http://www.nisc.nih.gov/
           Contact: nisc.mgc@nih.gov
           Akhtar, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
           Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
           Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
           Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
           Maduro, Q.U., Mastello, C., Maskell, B., Mastrian, S.D., McCloskey, J.C.,
           McDowell, J., Pearson, R., Stantrilop, S., Thomas, P.J., Touchman, J.W.,
           Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
           Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
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This clone was selected for full length sequencing because it
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BASE COUNT      530 a      467 c      440 g      423 t
ORIGIN
Query Match      67.1%; Score 573.4; DB 10; Length 1860;
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Search completed: March 19, 2003, 13:08:16  
Job time : 31308 secs



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PI	Hillman JL, Shah P;
DR	WPI; 1998-557119/47.
XX	P-PsDB; AAM81101.
PT	Human mitochondrial adenylate kinase, HMAK - useful e.g. to treat
PT	neurological disorders such as Alzheimer's and screen for
XX	antagonists for treatment of cancer or immunological disorders
PS	Claim 1; Fig 1; 63pp: English.
CC	
CC	The human mitochondrial adenylate kinase (HMAK) (854bp) gene encodes a
CC	protein of 227 amino acids ) can be administered therapeutically,
CC	especially by expressing encoding polypeptides, to treat neurological
CC	disorders e.g. Alzheimer's disease, Huntington's disease, epilepsy. It
CC	can be combined with a suitable carrier in pharmaceutical compositions,
CC	which can be administered to treat such disorders. HMAK was shown to
CC	have chemical and structural homology with adenylate kinase isozyme 3
CC	(AK3) from cow, rat and human (92, 91 and 57 % identity respectively)
CC	and was expressed in e.g. cancerous tissues, brain and neural tissues
CC	and tissues involved in inflammation and the immune response.
CC	Increased activity or expression was proposed to be associated with
CC	cancer and immunological disorders, and decreased activity/expression
CC	with the development of neurological disorders. Products of the above
CC	invention may be used in the diagnosis and treatment of the above
CC	diseases and disorders.
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DB	361 GAGCTTATCAATGACACAGTATTAACCTGAAATGTGCCCTTTGAGGTCAATTAAACAAC 420
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PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;				
XX					
DR	WPI: 2001-318749/34.				
XX					
PT	Primer sets for synthesizing polynucleotides, particularly the 5602				
PT	full-length cDNAs defined in the specification, and for the detection				
PT	and/or diagnosis of the abnormality of the proteins encoded by the				
PT	full-length cDNAs -				
XX					
PS	Claim 8; SEQ ID 12785; 2537bp + CD ROM; English.				
XX					
CC	The present invention describes primer sets for synthesizing 5602				
CC	full-length cDNAs defined in the specification. Where a primer set				
CC	comprises: (a) an oligo-dT primer and an oligonucleotide complementary				
CC	to the complementary strand of a polynucleotide which comprises one of				
CC	the 5602 nucleotide sequences defined in the specification, where the				
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination				
CC	of an oligonucleotide comprising a sequence complementary to the				
CC	complementary strand of a polynucleotide which comprises a 5'-end				
CC	sequence and an oligonucleotide comprising a sequence complementary to a				
CC	polynucleotide which comprises a 3'-end sequence, where the				





[illegible]

PT		disorders, immune diseases, inflammation or blood disorders
PS		
PX		
XX		
CC	Claim 1; Page 291-292; 721pp; English.	
CC	This sequence represents a nucleic acid molecule designated Gene 58 from	
CC	the human cDNA clone HHHN61 (deposited as clone ATCC 97899 and ATCC	
CC	209045) which encodes a secreted human protein. The gene can be used to	
CC	generate fusion proteins by linking to the gene to a human	
CC	immunoglobulin Fc portion (e.g., AAV5502) for increasing the stability of	
CC	the fused protein as compared to the human protein only.	
CC	The invention relates to 186 novel genes and their fragments (nucleic	
CC	acid sequences: AAV59511-V59812; amino acid sequences AAH74731-W75026)	
CC	which are useful for preventing, treating or ameliorating medical	
CC	conditions e.g. by protein or gene therapy. Also, pathological conditions	
CC	can be diagnosed by determining the amount of the new polypeptides in a	
CC	sample or by determining the presence of mutations in the new	
CC	polynucleotides. Specific uses are described for each of the 186	
CC	polynucleotides, based on which tissues they are most highly expressed in	
CC	(see AAV59511 for described uses).	
SQ	Sequence 1751 BP; 531 A; 353 C; 379 G; 485 T; 3 other;	
	Query Match 97.8%; Score 835.2; DB 19; Length 1751;	
	Best Local Similarity 99.2%; Pred. No. 3.5e-236;	
	Matches 848; Conservative 0; Mismatches 6; Indels 1; Gaps 1	
OY	1 GCCAAGGCCAAAGCCCTGTATACCGGCGGGT-GGGCCTCAGTCGCGGCATGGGGGCG 59	
Db		
	44 GGCCAGGCCAAAGCCCTGTATACCGGCGGGTGGGCTCAGTCGCGGCATGGGGGCG 103	
OY	60 TC CGCGGCGGCTCTCGAGCGGTGATCATAGGGGGCCCCGGCTCGGGCAAGGGCACCCGTG 119	
Db		
	104 TC CGCGGCGGCTCTCGAGCGGTGATCATAGGGGGCCCCGGCTCGGGCAAGGGCACCCGTG 163	
OY	120 TCGTGCGCGATACTACACACTTCGAGCTGAAGCACCTTCCAAGCGGGAGCTGCTCGG 179	
Db		
	164 TCGTGCGCGATACTACACACTTCGAGCTGAAGCACCTTCCAAGCGGGAGCTGCTCGG 223	
OY	180 GACAACATCTCTCGGGGCGACAGAATTTGGCGATTAGCCAGACGCTTTCATTGACCAAGG 239	
Db		
	224 GACAACATCTCTCGGGGCGACAGAATTTGGCGATTAGCCAGACGCTTTCATTGACCAAGG 283	
OY	240 AAAGTCATCCAGATGATGTCATGACTCGGGCTGGCCCTTCATGAGCTGAAAATCTCAC 299	
Db		
	284 AAAGTCATCCAGATGATGTCATGACTCGGGCTGGCCCTTCATGAGCTGAAAATCTCAC 343	
OY	300 CAGTATAGCTGGCTGTGGATGGTTTTCCAAGACACTTCCACAGGACGAACCCCTAGAT 359	
Db		
	344 CAGTATAGCTGGCTGTGGATGGTTTTCCAAGACACTTCCACAGGACGAACCCCTAGAT 403	
OY	360 AGAGCTTATCAATGACACAGTAGTAATCACTGAATGTCCTTTGAGGTCAATTAAACA 419	
Db		
	404 AGAGCTTATCAATGACACAGTAGTAATCACTGAATGTCCTTTGAGGTCAATTAAACA 463	
OY	420 GCCTTACTGCTCGTGATTATCCCGCAGTGGCCGAGTCTATPAACTTGAATTCAAC 479	
Db		
	464 GCCTTACTGCTCGTGATTATCCCGCAGTGGCCGAGTCTATPAACTTGAATTCAAC 523	
OY	480 CCTCCCAAACCTGTGGGCAATTGATGACTGGGGAGCCTCTCAATTCAGGTAGAGAT 539	
Db		
	524 CCTCCCAAACCTGTGGGCAATTGATGACTGGGGAGCCTCTCAATTCAGGTAGAGAT 583	
OY	540 GATTAACCAAGAGAGGTTATCAAGAGACTAAAGGCTTATGAGACCACAAACAGNCAGTC 599	
Db		
	584 GATTAACCAAGAGAGGTTATCAAGAGACTAAAGGCTTATGAGACCACAAACAGCCAGTC 643	
OY	600 CTGNATATTACAGAAAAAAGGGGTGCTGAAACATTCCTCCGGAACAGAAACCAACAG 659	
Db		
	644 CTGNATATTACAGAAAAAAGGGGTGCTGAAACATTCCTCCGGAACAGAAACCAACAG 703	
OY	660 ATTGGCCCTATGATATATGCTTTCTCTACAACTAAAGTTCCACAAAGAACCGAAGACT 719	
Db		
	704 ATTGGCCCTATGATATATGCTTTCTCTACAACTAAAGTTCCACAAAGAACCGAAGACT 763	



QY	720	TCACATTCACGACGAGAGAAAGTGTGTACTATTATTAAGTAAGATGGCAAACTCTT	779
Db	764	TCACATTCACGACGAGAGAAAGTGTGTACTATTATTAAGTAAGATGGCAAACTCTT	823
QY	780	AGTCCCTGCATTAGAAGCTGCTTTTCCCTAAGACCTCTGTATGTATGAATCTTGTGAA	839
Db	824	AGTCCCTGCATTAGAAGCTGCTTTTCCCTAAGACCTCTGTATGTATGAATCTTGTGAA	883
QY	840	ATTATATTACTTTTA	854
Db	884	ATTATATTACTTTTA	898
RESULT 4			
AAH14427			
ID	AAH14427	standard; CDNA; 2642 BP.	
XX	AAH14427;		
DT	26-JUN-2001	(first entry)	
XX	Human cDNA sequence SEQ ID NO:11882.		
DE	Human cDNA sequence SEQ ID NO:11882.		
XX	Human: primer; detection; diagnosis; antisense therapy; gene therapy; ss		
KW	Human: primer; detection; diagnosis; antisense therapy; gene therapy; ss		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	EPI074617-A2.		
PN	EPI074617-A2.		
XX	07-FEB-2001.		
PD	07-FEB-2001.		
XX	28-JUL-2000; 2000EP-0116126.		
PE	28-JUL-2000; 2000EP-0116126.		
PR	29-JUL-1999; 99JP-0248036.		
XX	27-AUG-1999; 99JP-0300253.		
PR	11-JAN-2000; 2000JP-0118776.		
PR	02-MAY-2000; 2000JP-0183767.		
PR	09-JUN-2000; 2000JP-0241899.		
XX	(HELI-) HELIX RES INST.		
PA	(HELI-) HELIX RES INST.		
XX	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;		
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;		
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;		
XX	WPI: 2001-318749/34.		
XX	Primer sets for synthesizing polynucleotides, particularly the 5602		
PT	full-length cDNAs defined in the specification, and for the detection		
PT	and/or diagnosis of the abnormality of the proteins encoded by the		
PT	full-length cDNAs -		
XX	Claim 8; SEQ ID 11882; 2537bp + CD ROM; English.		
XX	The present invention describes primer sets for synthesizing 5602		
CC	full-length cDNAs defined in the specification, where a primer set		
CC	comprises: (a) an oligo-dT primer and an oligonucleotide complementary		
CC	to the complementary strand of a polynucleotide which comprises one of		
CC	the 5602 nucleotide sequences defined in the specification, where the		
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination		
CC	of an oligonucleotide comprising a sequence complementary to the		
CC	complementary strand of a polynucleotide which comprises a 5'-end		
CC	sequence and an oligonucleotide comprising a sequence complementary to a		
CC	polynucleotide which comprises a 3'-end sequence, where the		
CC	oligonucleotide comprises at least 15 nucleotides and the combination of		
CC	the 5'-end sequence/3'-end sequence is selected from those defined in		
CC	the specification. The primer sets can be used in antisense therapy and		
CC	in gene therapy. The primers are useful for synthesizing polynucleotides		
CC	particularly full-length cDNAs. The primers are also useful for the		
CC	detection and/or diagnosis of the abnormality of the proteins encoded by		
CC	the full-length cDNAs. The primers allow obtaining of the full-length		
CC	cDNAs easily without any specialised methods. AAH03166 to AAH13628 and		
CC	AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to		

CC AAB55893 represent human amino acid sequences; and AAH13629 to AAH13632  
CC represent oligonucleotides, all of which are used in the exemplification  
CC of the present invention.

Sequence 2642 BP; 803 A; 503 C; 549 G; 787 T; 0 other;

Query Match	97.88;	Score 835.2;	DB 22;	Length 2642;
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Best Local Similarity  55.28;  Freq. NO. 4.4e-250;
Matches  848;  Conservative  0;  Mismatches  6;  Indels  1;  Gaps  1;

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Matches	848;	Conservative	0;	Mismatches	6;	Indels	1;	Gaps	1;
---------	------	--------------	----	------------	----	--------	----	------	----

QY 1 GCCANGCCCAAGCCCTGGTACCCGGGGGTG-GGGCTCAGTCTGCGGCCATGGGGCG 59

Db 90 GCCCAGCCAAAGCCCTGTTACCCGCCGGTGCGGGCCTCAGTCTCGGCCCATGGGGCG 149

60 TCCGCGGCTGCTGCGAGCGGTGATCATGGGGGCCCCGGGCTCGGGCAAGGCAACCGTG 119

Db 150 TCCGCGCGCTGCTGCGAGCGGTGATCATGGGGGCCCCGGCTCGGGCAAGGCAACCGTG 209

120 TCGTCGCGCATCACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGACCTGCTCCGG 179

Db 210 TCGTCGCGCATCCTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGACCTGCTCCGG 269

**Ov 180 GACGACATGCGCGCGCGCACGAAATGCGCGCGCGCAAGCGCTTTCATTGACGCACAAGGG 239**

D6  
370 CACCAATCCCCCAACAATTCCCCCAACCACCCCAACC  
|||||  
|||||

[illegible]

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[illegible]

DD 430 AGAGCCTATTCAGATCGACACAGTGAATATACCTGAAATGTCCTTATGAGGTCATATATACATAATGCTG

420 CCCCCTACCTGCTGGCTGGATTCATCCCGCCAGTGGCCGAGTCTATACCAATTGAATTCAC 4/5

Db 510 GCGCTTACTGCTGGCTGGATTCAATCCCGCCAGTGGCCGAGTCTATACAAATTGAAATTCAC 565

QY 480 CCTCCCAAACTGTGGGCAATTGATGACCTGACTGGGGAGCCCTCTCATTCAGCGTGAGGAT 533

Db 570 CCTCCAAACTGTGGGATGATGACCTGACTGGGGAGCCCTCTCATTCAGCGTGAGGAT 6229

QY 540 GATAAACCAGAGCGTTATCAAGAGACTAAAGGCTTATGAAGACCAACAAGNCAGTC 599

Db 630 GATAAACGAGACGGTTATCAAGAGACTAAAGGCTTATGAAGACCAACAAGCCAGTC 689

600 CTGGNATATTACCAGAAAAAGGGTCTGGAACATTTCTCCGGAACAGAAACCAACAAG 659

Db 690 CTGGAATATTACCAGAAAAAGGGTCTGGAACATCTCCGGAACAGAAACCAACAAG 749

660 ATTTGCCCTATGTATGCTTCTCCTACAACTAAAGTCCACAAGAAGCCAGAAGCT 719

Db 750 ATTTGCCCTATGTATATGCTTTCCTACAACCTAAAGTTCACACAAGAAGCCAGAAGCT 809

QY 720 TCAGTACTCCATGAGGAGAAATGTGTCTAACTATTAACTAGTAAGATGGGCAACCTCCT 779

Dp 810 TCACTTACTCCATGAGGAGAAATGCTGCTAACTATTATAGTAAGATGGCAACCTCCT 869

780 AGTCCCTGCATTAGAGCTGCTTTCTTAAGACTTCTAGTATGTATGAATCTTTGAAA 839

870 AGTCCCTTGCATTTTACGAAGCTGCTTTTCCCTAAGACTTTCATGTAATGTAATGAATTCCTTTGAAA 929

07 840 277277ACCTTTA 954

[illegible]

RESULT 5  
2.0000000

XX	AAH33296 standard; cDNA; 2765 BP.
XX	AAH33296;
XX	03-SEP-2001 (first entry)
XX	
DE	Human colon cancer antigen encoding cDNA SEQ ID NO:352.
XX	
KW	Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW	colorectal carcinoma; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200122920-A2.
XX	
PD	05-APR-2001.
XX	
PE	28-SEP-2000; 2000WO-US26524.
XX	
PR	29-SEP-1999; 99US-0157137.
PR	03-NOV-1999; 99US-0163280.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Ruben SM, Barash SC, Birse CE, Rosen CA;
XX	
DR	WPI: 2001-235357/24.
DR	P-PSDB; AAG73865.
XX	
PT	Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX	useful for preventing, diagnosing and/or treating colorectal cancers -
XX	Claim 1; Page 2462-2463; 9803pp; English.
XX	
CC	AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC	cancer-associated nucleic acid molecules (N) and proteins (P), where
CC	the proteins are collectively known as colon cancer antigens. The colon
CC	cancer antigens have cytostatic activity and can be used in gene
CC	therapy and vaccine production. N and P may be used in the prevention,
CC	diagnosis and treatment of diseases associated with inappropriate P
CC	expression. For example, N and P may be used to treat disorders
CC	associated with decreased expression by rectifying mutations or deletions
CC	in a patient's genome that affect the activity of P by expressing
CC	inactive proteins or to supplement the patients own production of P.
CC	Additionally, N may be used to produce the colon cancer-associated Ps,
CC	by inserting the nucleic acids into a host cell and culturing the cell
CC	to express the proteins. N and P can be used in the prevention, diagnosis
CC	and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC	and AAG77789 represent sequences used in the exemplification of the
CC	present invention.
CC	N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC	missing at time of publication, meaning no sequences are present for
CC	SEQ ID NO:1027 to 1052, 7921 and 7922.
XX	
XX	Sequence 2765 BP; 872 A; 523 C; 575 G; 793 T; 2 other;

Query Match	Best Local Similarity	97.88;	Score 835.2;	DB 22;	Length 2765;
Matches	848;	Conservative	0;	Mismatches 6;	Indels 1;
					Gaps 1;
QY	1	GCCAGGCCAAAGCCCTGTGTAACCGCGCGGTTG-GGCCCTCAGTGTCCGGCCATGGGGCG	59		
Db	146	GGCCAGGGCCAAAGCCCTGTGTAACCGCGGGGTGGGGCCCTCAGTGTGGGCCATGGGGGGG	205		
QY	60	TCCCGCGGCTGTGTCCAGCGCGGTGATCATGGGGGGCCCCGGGCTGGGGCAAGGGCACCGTG	119		
Db	206	TCCCGCGGCTGTGTCCAGCGCGGTGATCATGGGGGGCCCCGGGCTGGGGCAAGGGCACCGGTG	265		
QY	120	TGTGTGGGCATCACTACACACTTGTGAGGTGAAGCACTCTCCAGGGGGGACCTGTGTCGG	179		
Db	266	TGTGTGGGCATCACTACACACTTGTGAGGTGAAGCACTCTCTCAGCGGGGACCTGTCTCCGG	325		
QY	180	GACAACTATGCTGGGGGGCACAGAAATTGGCGTGTTAAGCCAAGGCTTTATCATTTGACCAAGG	239		

[illegible]



XX 26-DEC-2000; 2000MO-US34263 .  
 PF  
 XX 21-JAN-2000; 2000US-0488725 .  
 PR 25-APR-2000; 2000US-0552317 .  
 PR 09-JUL-2000; 2000US-0598042 .  
 PR 19-JUL-2000; 2000US-0620312 .  
 PR 03-AUG-2000; 2000US-0653450 .  
 PR 14-SEP-2000; 2000US-0662191 .  
 PR 19-OCT-2000; 2000US-0693036 .  
 PR 29-NOV-2000; 2000US-0727344 .  
 XX  
 PA (HYSE-) HYSEQ INC.  
 PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao Q, Zhou P, Goodlich R, Drmanac RT;  
 DR WPI: 2001-442253/47 .  
 DR P-PSDB; AAM40685 .  
 XX  
 XX Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 PS  
 PS Claim 1; SEQ ID NO 3830; 10078bp; English.  
 XX  
 XX The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic  
 CC immunosuppressant and cyostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 XX  
 SQ Sequence 2432 BP; 771 A; 436 C; 489 G; 736 T; 0 other;

Query Match 96.0%; Score 820; DB 22; Length 2432;  
 Best Local Similarity 99.8%; Pred. No. 1.3e-231;  
 Matches 820; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 33 GGGCCTCAAGTCTGCGGCAATGGGGGCTCCGCGGCTGCTCGAGCGGTGATCATGGGG 92  
 |||||||  
 DB 19 GGGCCTCAAGTCTGCGGCAATGGGGGCTCCGCGGCTGCTCGAGCGGTGATCATGGGG 78  
 |||||||  
 QY 93 GGGCCTCAAGTCTGCGGCAATGGGGGCTCCGCGGCTGCTCGAGCGGTGATCATGGGG 152  
 |||||||  
 DB 79 GGGCCTCAAGTCTGCGGCAATGGGGGCTCCGCGGCTGCTCGAGCGGTGATCATGGGG 138  
 |||||||  
 QY 153 GGGCCTCAAGTCTGCGGCAATGGGGGCTCCGCGGCTGCTCGAGCGGTGATCATGGGG 212  
 |||||||  
 DB 139 GGGCCTCAAGTCTGCGGCAATGGGGGCTCCGCGGCTGCTCGAGCGGTGATCATGGGG 198  
 |||||||  
 QY 213 GGGCCTCAAGTCTGCGGCAATGGGGGCTCCGCGGCTGCTCGAGCGGTGATCATGGGG 272  
 |||||||  
 DB 199 GGGCCTCAAGTCTGCGGCAATGGGGGCTCCGCGGCTGCTCGAGCGGTGATCATGGGG 258  
 |||||||  
 QY 273 GGGCCTCAAGTCTGCGGCAATGGGGGCTCCGCGGCTGCTCGAGCGGTGATCATGGGG 332  
 |||||||  
 DB 259 GGGCCTCAAGTCTGCGGCAATGGGGGCTCCGCGGCTGCTCGAGCGGTGATCATGGGG 318  
 |||||||  
 QY 333 GGGCCTCAAGTCTGCGGCAATGGGGGCTCCGCGGCTGCTCGAGCGGTGATCATGGGG 392  
 |||||||  
 DB 319 GGGCCTCAAGTCTGCGGCAATGGGGGCTCCGCGGCTGCTCGAGCGGTGATCATGGGG 378  
 |||||||

QY 393 AATGTCCTCTTGGAGTCAATTAACAGCCCTTACTGCTGCGGTGATTCATCCGGCACT 452  
 |||||||  
 DB 379 AATGTCCTCTTGGAGTCAATTAACAGCCCTTACTGCTGCGGTGATTCATCCGGCACT 438  
 |||||||  
 QY 453 GGGCCTCAAGTCTGCGGCAATGGGGGCTCCGCGGCTGCTCGAGCGGTGATCATGGGG 512  
 |||||||  
 DB 439 GGGCCTCAAGTCTGCGGCAATGGGGGCTCCGCGGCTGCTCGAGCGGTGATCATGGGG 498  
 |||||||  
 QY 513 GGGGAGCCTCTCATTCAGGCTGAGTGAATTAACAGAGCGGTTCATGAGACTAAAG 572  
 |||||||  
 DB 499 GGGGAGCCTCTCATTCAGGCTGAGTGAATTAACAGAGCGGTTCATGAGACTAAAG 558  
 |||||||  
 QY 573 GCTTATGAAGACCAACCAAGCAGTCTGATTAATTAACAGAGAGAGAGAGAGAGAGAG 632  
 |||||||  
 DB 559 GCTTATGAAGACCAACCAAGCAGTCTGATTAATTAACAGAGAGAGAGAGAGAGAGAG 618  
 |||||||  
 QY 633 ACATTCCTCCGGAACAGAAACCAAGATTTGGCCCTATGATATGCTTCTTCTTCAAACT 692  
 |||||||  
 DB 619 ACATTCCTCCGGAACAGAAACCAAGATTTGGCCCTATGATATGCTTCTTCTTCAAACT 678  
 |||||||  
 QY 693 AAAGTCCCAACCAAG 752  
 |||||||  
 DB 679 AAAGTCCCAACCAAG 738  
 |||||||  
 QY 753 AATTAATGAAGATGAGGCAACCTCTTACTGCTTGTGATTAAGAGCTCTTCTTCTTAA 812  
 |||||||  
 DB 739 AATTAATGAAGATGAGGCAACCTCTTACTGCTTGTGATTAAGAGCTCTTCTTCTTAA 798  
 |||||||  
 QY 813 CTCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 854  
 |||||||  
 DB 799 CTCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
 |||||||

## RESULT 8

AA158055  
 ID AA158055 standard; cDNA; 2421 BP.

AA158055;

22-OCT-2001 (first entry)

Human polynucleotide SEQ ID NO 258.

Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer;  
 peripheral nervous system; neuropathy; central nervous system; CNS;  
 Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 leukaemia; ss.

Homo sapiens.

WO200153312-A1.

26-JUL-2001.

26-DEC-2000; 2000MO-US34263.

21-JAN-2000; 2000US-0488725 .  
 25-APR-2000; 2000US-0552317 .  
 09-JUL-2000; 2000US-0598042 .  
 19-JUL-2000; 2000US-0620312 .  
 03-AUG-2000; 2000US-0653450 .  
 14-SEP-2000; 2000US-0662191 .  
 19-OCT-2000; 2000US-0693036 .  
 29-NOV-2000; 2000US-0727344 .  
 XX  
 XX (HYSE-) HYSEQ INC.

PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao Q, Zhou P, Goodlich R, Drmanac RT;

DR MPI: 2001-442253/47.  
DR P-PSDB: AAM38899.  
XX Novel nucleic acids and polypeptides, useful for treating disorders  
PT such as central nervous system injuries -  
XX  
XX  
PS Claim 1: SEQ ID NO 258; 10078bp; English.  
XX  
CC The invention relates to human nucleic acids (AA157798-AA161369) and  
CC the encoded polypeptides (AAM38642-AA442213) with neurotrophic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification.  
XX  
SQ Sequence 2421 BP; 768 A; 431 C; 487 G; 735 T; 0 other:  
Query Match 95.6%; Score 816.8; DB 22; Length 2421;  
Best Local Similarity 99.5%; Pred. No. 1.1e-230;  
Matches 818; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
XX  
OY 33 GGGGCTCATGTCGGCCATGGGGGGGCTCCGGCGCTGCTGGAGCGGATCATGGGG 92  
DB 19 GGGGCTCATGTCGGCCATGGGGGGGCTCCGGCGCTGCTGGAGCGGATCATGGGG 78  
OY 93 GGGGCGGCTCGGGGCAAGGGGCAAGGCGTGTGCGGATCATGAGCTCGAGCTGAAG 152  
DB 79 GGGGCGGCTCGGGGCAAGGGGCAAGGCGTGTGCGGATCATGAGCTCGAGCTGAAG 138  
OY 153 CACCTCTCCAGCGGGGACCTGCTCGGGGCAACATGCTGGGGGCAAGAAATGGCGTG 212  
DB 139 CACCTCTCCAGCGGGGACCTGCTCGGGGCAACATGCTGGGGGCAAGAAATGGCGTG 198  
OY 213 TAGGCAAGGCTTTCATGACCAAGGAAACATCATCCGATGATGATCATGATCGGCTG 272  
DB 199 TAGGCAAGGCTTTCATGACCAAGGAAACATCATCCGATGATGATCATGATCGGCTG 258  
OY 273 GGCCTTCATGAGCTGAAAAATCTCACCCAGTATAGCTGGCTGTTGGATGTTTCCAAAG 332  
DB 259 GGCCTTCATGAGCTGAAAAATCTCACCCAGTATAGCTGGCTGTTGGATGTTTCCAAAG 318  
OY 333 ACACCTCCACAGGCAAGACCCCTAGATAGCTTATCAATGACACAGATGATTAACCTG 392  
DB 319 ACACCTCCACAGGCAAGACCCCTAGATAGCTTATCAATGACACAGATGATTAACCTG 378  
OY 393 AATGTCGCTTTGAGTGCATTTAAACAAGCGCTTACTGCTGCTGGATGTTCCCGCAGT 452  
DB 379 AATGTCGCTTTGAGTGCATTTAAACAAGCGCTTACTGCTGCTGGATGTTCCCGCAGT 438  
OY 453 GGGCGAGTGTATTAACATTTGAACCTCCCAAAATCTGGGCAATGATGACTGACT 512  
DB 439 GAGCGAGTGTATTAACATTTGAATCAACCTCCCAAAATCTGGGCAATGATGACTGACT 498  
OY 513 GGGGAGGCTCTCATTCAGCGTGAGATGATTAACCAAGACGCTTATCAAGACATTAAG 572  
DB 499 GGGGAGGCTCTCATTCAGCGTGAGATGATTAACCAAGACGCTTATCAAGACATTAAG 558  
OY 573 GCTTATGAAGACCAACAAGACGCTCGTGNATATTACAGAAAAAAGGGGCTGGAA 632  
DB 559 GCTTATGAAGACCAACAAGACGCTCGTGNATATTACAGAAAAAAGGGGCTGGAA 618  
OY 633 ACATTCGCGGAACAGAAACCAAGATTTGGCCCTATGATATGATGTTCTTCAAACT 692  
XX

DB 619 ACATTCGCGGAACAGAAACCAACAGATTTGGCCCTATGATATGCTTCTCAAACT 678  
OY 693 AAAGTTCACAAAGAACCCAGAAAGCTTCAGTTACTCATGAGAGAAATGTGTAACT 752  
DB 679 AAAGTTCACAAAGAACCCAGAAAGCTTCAGTTACTCATGAGAGAAATGTGTAACT 738  
OY 753 ATTAATAGTAAAGTGGGCAACCTCCAGTCTGCTGATTTAGAAAGCTTTCCTAGA 812  
DB 739 ATTAATAGTAAAGTGGGCAACCTCCAGTCTGCTGATTTAGAAAGCTTTCCTAGA 798  
OY 813 CTCTAGTATGATGTAATCTTTGAAATATATTAATCTTTA 854  
DB 799 CTCTAGTATGATGTAATCTTTGAAATATATTAATCTTTA 840  
RESULT 9  
ID AAH14215 standard; cDNA; 2394 BP.  
XX AAH14215:  
AC 26-JUN-2001 (first entry)  
XX  
DT 26-JUN-2001 (first entry)  
XX  
DE Human cDNA sequence SEQ ID NO:11491.  
XX  
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
XX Homo sapiens.  
OS  
XX  
PN EP1074617-A2.  
XX  
PD 07-FEB-2001.  
XX  
PF 28-JUL-2000; 2000BP-0116126.  
XX  
PR 29-JUL-1999; 99JP-0248036.  
PR 27-AUG-1999; 99JP-0300253.  
PR 11-JAN-2000; 2000JP-0118776.  
PR 02-MAY-2000; 2000JP-0183767.  
PR 09-JUN-2000; 2000JP-0241899.  
XX  
PA (HELI-) HELIX RES INST.  
XX  
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
DR MPI: 2001-318749/34.  
XX  
PT Primer sets for synthesizing polynucleotides, particularly the 5602  
PT full-length cDNAs defined in the specification, and for the detection  
PT and/or diagnosis of the abnormality of the proteins encoded by the  
PT full-length cDNAs -  
XX  
PS Claim 8: SEQ ID 11491; 2537pp + CD ROM; English.  
XX  
CC The present invention describes primer sets for synthesizing 5602  
CC full-length cDNAs defined in the specification. Where a primer set  
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
CC to the complementary strand of a polynucleotide which comprises one of  
CC the 5602 nucleotide sequences defined in the specification, where the  
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
CC of an oligonucleotide comprising a sequence complementary to the  
CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a  
CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in  
CC the specification. The primer sets can be used in antisense therapy and  
CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences: AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13632 to  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.

SO Sequence 2394 BP; 760 A; 428 C; 477 G; 729 T; 0 other;

Query Match 95.6%; Score 816; DB 22; Length 2394;  
 Best Local Similarity 99.8%; Pred. No. 2e-230;  
 Matches 816; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

OY 37 CTCAGCTGCGGCCCATGCGGGCGTCCGCGCGCTGCTCGAGCGGTGATCATGGGGCCC 96
DB 1 CTCAGCTGCGGCCCATGCGGGCGTCCGCGCGCTGCTCGAGCGGTGATCATGGGGCCC 60
OY 97 CGGGGTCGGGGAAGGCAACCGTGTGCGGCATCACTACACATTCGAGCGTGAAGCAC 156
DB 61 CGGGGTCGGGGAAGGCAACCGTGTGCGGCATCACTACACATTCGAGCGTGAAGCAC 120
OY 157 TCTCCAGCGGGGACCTGCTCCGGGCAACATGCTCGCGGGCACAGAAATTTGGCGTTAG 216
DB 121 TCTCCAGCGGGGACCTGCTCCGGGCAACATGCTCGCGGGCACAGAAATTTGGCGTTAG 180
OY 217 CCAAGGCTTTCTATTGACCAAGGAAATCTATCCAGATGATGCTGACTCGGCTGGCCC 276
DB 181 CCAAGGCTTTCTATTGACCAAGGAAATCTATCCAGATGATGCTGACTCGGCTGGCCC 240
OY 277 TTCATGAGCTGAAAAATCTCACCCAGTATAGTGTGCTGTGATGTTTCCAAAGGACAC 336
DB 241 TTCATGAGCTGAAAAATCTCACCCAGTATAGTGTGCTGTGATGTTTCCAAAGGACAC 300
OY 337 TTCACAGGCGACAGACCCCTAGATAGAGCTTATCAGATCGACACAGTGAATTAAGTATG 396
DB 301 TTCACAGGCGACAGACCCCTAGATAGAGCTTATCAGATCGACACAGTGAATTAAGTATG 360
OY 397 TGGCCCTTTGAGGTCATTAACAAGCCCTTACTGCTGCTGATTCATCCCGCAGTGGCC 456
DB 361 TGGCCCTTTGAGGTCATTAACAAGCCCTTACTGCTGCTGATTCATCCCGCAGTGGCC 420
OY 457 GAGTATTAACATTAATTCACACCCCTCAAAAGTGGGGCATGATGACCTGAGTGGGG 516
DB 421 GAGTATTAACATTAATTCACACCCCTCAAAAGTGGGGCATGATGACCTGAGTGGGG 480
OY 517 AGCCTCTCATTCAGCGTGGAGTGTAAACAGAGACGGTTATCAAGAGACTAAAGGCTT 576
DB 481 AGCCTCTCATTCAGCGTGGAGTGTAAACAGAGACGGTTATCAAGAGACTAAAGGCTT 540
OY 577 ATGAAGACCAACAAGNCAGTCTGNNATTTACCCAGAAAAAGGGGTCTGGAACAT 636
DB 541 ATGAAGACCAACAAGNCAGTCTGNNATTTACCCAGAAAAAGGGGTCTGGAACAT 600
OY 637 TCTCGGAACAGAAACCAACAGATTTGGCCCTATGTATGCTTCCACAAACTAAAG 696
DB 601 TCTCGGAACAGAAACCAACAGATTTGGCCCTATGTATGCTTCCACAAACTAAAG 660
OY 697 TTCCACAAGAAGCCAGAAGCTTCACTACTCATGAGAGAAATGTGTACTATTA 756
DB 661 TTCCACAAGAAGCCAGAAGCTTCACTACTCATGAGAGAAATGTGTACTATTA 720
OY 757 ATAGTAAGTGGGCAAACTCTAGTCTTGATTTAGAGCTGTTTCTTAAGACTTC 816
DB 721 ATAGTAAGTGGGCAAACTCTAGTCTTGATTTAGAGCTGTTTCTTAAGACTTC 780
OY 817 TAGTATGATGAATCTTTGAATAATTAATTAATTTA 854
DB 781 TAGTATGATGAATCTTTGAATAATTAATTAATTTA 818

```

RESULT 10  
 AAH47197  
 ID AAH47197 standard; CDNA: 2394 BP.  
 XX  
 AC AAH47197;

XX 30-NOV-2001 (first entry)  
 DR  
 XX  
 DE Human adenylate kinase 3 (AK3)-like protein encoding cDNA.

XX Adenylate kinase 3-like protein; AK3-like protein; AK3; cell morphology;  
 KW MELAS; central nervous system disorder; epilepsy; skeletal muscle;  
 KW muscle disease; electron transfer disorder; Leber disease; human;  
 KW diabetes mellitus; Pearson disease; Parkinson's disease;  
 KW metabolism disorder; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 15..698

FT /tag= "a"

FT /product= "AK3-like protein"

PN WO200109346-A1.

PD 08-FEB-2001.

PN 28-JUL-2000; 2000WO-JP05066.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 18-OCT-1999; 99US-0159590.

PR 11-JAN-2000; 2000JP-0118776.

PR 17-FEB-2000; 2000US-0183322.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Hayashi K, Saito K, Yamamoto J, Ishii S;

PI Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Ihara S, Nakae H;

PI Nishikawa T, Kimura K;

XX WPI: 2001-564737/63.

DR P-PSDB; AAB85885.

XX New gene encoding an adenylate kinase 3-like protein, and the protein

PT and antibodies to it, useful for diagnosis of brain disease e.g.

PT epilepsy, muscle disease, genetic disorder, diabetes

XX Claim 1; Page 32-34; 41pp; Japanese.

XX The invention relates to a cDNA (clone C-NT2RP2000329) encoding a novel

CC adenylate kinase 3 (AK3)-like protein. C-NT2RP2000329 has functions of

CC converting extracellular signals into intracellular signals and changing

CC cell morphology. The AK3-like protein, polynucleotides and antibodies are

CC useful in the investigation of diseases such as MELAS (cerebral accident

CC condition with hyperlactacidemia), central nervous system disorder,

CC epilepsy, skeletal muscle conditions, muscle disease, electron transfer

CC disorders, Leber disease, diabetes mellitus, Pearson disease, Parkinson's

CC disease, metabolism disorders. They are useful for developing diagnostics

CC and treatment agents. The present sequence represents a cDNA encoding a

CC human AK3-like protein of the invention.

SO Sequence 2394 BP; 760 A; 428 C; 477 G; 729 T; 0 other;

Query Match 95.6%; Score 816; DB 22; Length 2394;  
 Best Local Similarity 99.8%; Pred. No. 2e-230;  
 Matches 816; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

OY 37 CTCAGCTGCGGCCCATGCGGGCGTCCGCGCGCTGCTCGAGCGGTGATCATGGGGCCC 96
DB 1 CTCAGCTGCGGCCCATGCGGGCGTCCGCGCGCTGCTCGAGCGGTGATCATGGGGCCC 60
OY 97 CGGGGTCGGGGAAGGCAACCGTGTGCGGCATCACTACACATTCGAGCGTGAAGCAC 156
DB 61 CGGGGTCGGGGAAGGCAACCGTGTGCGGCATCACTACACATTCGAGCGTGAAGCAC 120
OY 157 TCTCCAGCGGGGACCTGCTCCGGGCAACATGCTCGCGGGCACAGAAATTTGGCGTTAG 216
DB 121 TCTCCAGCGGGGACCTGCTCCGGGCAACATGCTCGCGGGCACAGAAATTTGGCGTTAG 180

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Db 121 TCTCAGCGGGGACCTGCTCCGGACAACATGCTGCGGGGCACGAATTTGGCGTTAG 180
QY 217 CCAAGGCTTTCATTGACCAAGGAAACTCATCCAGATGATGTATATACTCGGGTGCC 276
    |||||
Db 181 CCAAGGCTTTCATTGACCAAGGAAACTCATCCAGATGATGTATATACTCGGGTGCC 240
QY 277 TTCATAGCTGAAAAATCTCACCCAGTATAGCTGGCTGTGGATGTTTCCAAAGACAC 336
    |||||
Db 241 TTCATAGCTGAAAAATCTCACCCAGTATAGCTGGCTGTGGATGTTTCCAAAGACAC 300
QY 337 TTCACACGCGAAGCCCTAGATAGACTTATCAGATGCACACAGTAACTGAATG 396
    |||||
Db 301 TTCACACGCGAAGCCCTAGATAGACTTATCAGATGCACACAGTAACTGAATG 360
QY 397 TGGCCTTGGAGTCATTAAACAACGCTTACTGCTCGCTGATCATCCGCCAGTGCC 456
    |||||
Db 361 TGGCCTTGGAGTCATTAAACAACGCTTACTGCTCGCTGATCATCCGCCAGTGCC 420
QY 457 GAGTCATAACATTGAATTCACCCCTCCAAAACCTGGGCAATGATGACCTGACGGG 516
    |||||
Db 421 GAGTCATAACATTGAATTCACCCCTCCAAAACCTGGGCAATGATGACCTGACGGG 480
QY 517 AGCCTCATTCAGCGTGAAGATGATTAACACAGACGCTTATCAAGACTAAAGCTT 576
    |||||
Db 481 AGCCTCATTCAGCGTGAAGATGATTAACACAGACGCTTATCAAGACTAAAGCTT 540
QY 577 ATGAAGACCAACAAGNCAGTCTGNNATTATTCAGAAAAAGGGGCTGTGAAACAT 636
    |||||
Db 541 ATGAAGACCAACAAGNCAGTCTGNNATTATTCAGAAAAAGGGGCTGTGAAACAT 600
QY 637 TCTCCGAGACAGAAACCAACAGATTTGGCCCTATGATATGCTTCTTCAACAACTAAG 696
    |||||
Db 601 TCTCCGAGACAGAAACCAACAGATTTGGCCCTATGATATGCTTCTTCAACAACTAAG 660
QY 697 TTCCACAAAAGACCAAGAACTTCACTACTCATGAGAGAAATGTGTAACTATTA 756
    |||||
Db 661 TTCCACAAAAGACCAAGAACTTCACTACTCATGAGAGAAATGTGTAACTATTA 720
QY 757 ATAGTAGATGAGCAACCTCTAGTCTTGCATTTAGAACTGCTTTTCTTAAGACTTC 816
    |||||
Db 721 ATAGTAGATGAGCAACCTCTAGTCTTGCATTTAGAACTGCTTTTCTTAAGACTTC 780
QY 817 TAGTAGTAGAATCTTTGAAAAATATATTAATCTTTTA 854
    |||||
Db 781 TAGTAGTAGAATCTTTGAAAAATATATTAATCTTTTA 818

RESULT 11
AAA60582
ID AAA60582 standard; cDNA; 751 BP.
XX
AC AAA60582:
XX
XX 20-OCT-2000 (first entry)
DE Human mitochondrial GTP:AMP phosphotransferase encoding cDNA SEQ ID NO:3.
XX
KM Human: mitochondrial GTP:AMP phosphotransferase; GTP3P; ribotide; ss.
XX
OS Homo sapiens.
XX
PN CN1249340-A.
XX
PD 05-APR-2000.
XX
PF 28-SEP-1998; 98CN-0119439.
XX
PR 28-SEP-1998; 98CN-0119439.
XX
PA (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.
XX
PI Yu L, Zhao Y, Bi A;
XX
```

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DR WPI: 2000-400718/35.
DR P-PSDB; AAB12440.
XX
PT Preparation of human mitochondrial matrix GTP : AMP phosphotransferase,
PT its encode sequence -
XX
PS Claim 1; Page 14; 20pp; Chinese.
XX
CC The present invention describes a new ribotide sequence of human gene,
CC that is, the cDNA sequence of human mitochondrial matrix GTP:AMP
CC phosphotransferase (GTP3P) and the encoded polypeptide. The present
CC sequence encodes human GTP3P.
XX
SQ sequence 751 BP; 211 A; 189 C; 186 G; 165 T; 0 other:

Query Match 85.58; Score 729.8; DB 21; Length 751;
Best Local Similarly 98.18; Pred. No. 3,2e-205;
Matches 737; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 51 ATGGGGGGGTGCGGCGGCTGCTGAGCGGTGATCATGGGGGCCGCGGCTCGGCAAG 110
    |||||
Db 1 ATGGGGGGCGGCGCGGCTGCTGAGCGGTGATCATGGGGGCCGCGGCTCGGCAAG 60
QY 111 GGCACCGTGTGTCGCGCATCTACACACTTCAGAGTGAAGACCTCTCCAGCGGGAC 170
    |||||
Db 61 GGCACCGTGTGTCGCGCATCTACACACTTCAGAGTGAAGACCTCTCCAGCGGGAC 120
QY 171 CTGCTCCGGGACAACATGCTCGGGGCGACAGAAATGGCGCTGTTAGCCAGGCTTTCAT 230
    |||||
Db 121 CTGCTCCGGGACAACATGCTCGGGGCGACAGAAATGGCGCTGTTAGCCAGGCTTTCAT 180
QY 231 GACCAAGGAAACATCCCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 290
    |||||
Db 181 GACCAAGGAAACATCCCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 291 AATCTCACCGATATAGCTGCTGTGGATGATGATGATGATGATGATGATGATGATGATGAT 350
    |||||
Db 241 AATCTCACCGATATAGCTGCTGTGGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 351 GCCCTAGTAGAGCTTATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 410
    |||||
Db 301 GCCCTAGTAGAGCTTATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 411 ATTAACAACAGCCTTACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 470
    |||||
Db 361 ATTAACAACAGCCTTACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 471 GAATTTCAACCTCTCCAAAACCTGTGGCATGATGATGATGATGATGATGATGATGATGATGAT 530
    |||||
Db 421 GAATTTCAACCTCTCCAAAACCTGTGGCATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 531 CGTGAAGATGATTAACAGAGACGTTATCAAGAGACTTAAGGCTTATGAAGACCAACA 590
    |||||
Db 481 CGTGAAGATGATTAACAGAGACGTTATCAAGAGACTTAAGGCTTATGAAGACCAACA 540
QY 591 AAGNCAGCTCGNATATTTACAGAAAAAAGGGGCTGGAAGAACTTCCGGGAACAGA 650
    |||||
Db 541 AAGNCAGCTCGNATATTTACAGAAAAAAGGGGCTGGAAGAACTTCCGGGAACAGA 600
QY 651 ACCAACAAGATTTGGCCCTATGATATGCTTTCTTACAACTAAAGTTCCACAAAGAAC 710
    |||||
Db 601 ACCAACAAGATTTGGCCCTATGATATGCTTTCTTCCACAACTAAAGTTCCACAAAGAAC 660
QY 711 CAGAAAGCTTCAAGTTACTCCATGAGAGAAATGTGTATTAATATGAAGATGGGC 770
    |||||
Db 661 CAGAAAGCTTCAAGTTACTCCATGAGAGAAATGTGTATTAATATGAAGATGGGC 720
QY 771 AAACCTCTAGTCTTGCATTTAGAGCTGC 801
    |||||
Db 721 AAACCTCTAGTCTTGCATTTAGAGCTGC 751

RESULT 12
```

AAC98376 standard; cDNA; 733 BP.  
ID AAC98376 standard; cDNA; 733 BP.  
XX AAC98376;  
AC AAC98376;  
XX  
DT 09-MAR-2001 (first entry)  
XX  
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:386.  
XX  
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
KW identification; cytosolic; cardiovascular; neuroprotective; vulnery;  
KW immunomodulatory; muscular; gynaecological; gastrointestinal;  
KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;  
KW neural disorder; immune system disorder; muscular disorder;  
KW reproductive disorder; gastrointestinal disorder; renal disorder;  
KW infectious disease; cardiovascular disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200055351-A1.  
XX  
PD 21-SEP-2000.  
XX  
PE 08-MAR-2000; 2000MO-US05883.  
XX  
PR 12-MAR-1999; 99US-0124270.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
PI WPI; 2000-587534/55.  
XX  
DR P-PSDB; AAB53619.  
XX  
PT Colon cancer associated gene sequences, referred to as colon cancer  
PT antigens, useful for the treatment, prevention, and diagnosis of colon  
PT disorders such as colon cancer -  
XX  
PS Claim 1; Page 849; 2104pp; English.  
XX  
XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,  
XX called human colon cancer antigens, given in AAB53234 to AAB54006. The  
XX human colon cancer antigens can have cytosolic, cardiovascular, muscular;  
XX neuroprotective, immunomodulatory, gynaecological, gastrointestinal,  
XX vulnerably, nephrotropic, antiinfective and antibacterial activities, and  
XX can be used in gene therapy. The colon cancer antigen polynucleotides,  
XX proteins and antibodies to the proteins are useful for the prevention,  
XX treatment and diagnosis of colon disorders, such as colon cancer. The  
XX polynucleotides may be used in diagnostics and research, such as for  
XX chromosome identification, and as hybridisation probes. The proteins  
XX may also be used to prevent diseases such as neural disorders, immune  
XX system disorders, muscular disorders, reproductive disorders,  
XX gastrointestinal disorders, wounds, renal disorders, infectious  
XX diseases, and cardiovascular disorders. AAC98764 to AAC98772 and  
XX AAB54007 represent sequences used in the exemplification of the present  
XX invention.  
XX  
SQ Sequence 733 BP; 213 A; 175 C; 173 G; 168 T; 4 other;  
Query Match 81.0%; Score 691.4; DB 21; Length 733;  
Best Local Similarity 97.5%; Pred. No. 7e-194;  
Matches 709; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

Db 121 ACAGAAATTGGCGTGTAGCCAGGAGGCTTTCATTGACCAAGGAAACTCATCCAGATGAT 180  
Qy 258 GTCATGACGCGGTGGCCCTTCATGACCTGAAATAATCTCACCCAGTATAGCTGGCTGTG 317  
Db 181 GTCATGACGCGGTGGCCCTTCATGACCTGAAATAATCTCACCCAGTATAGCTGGCTGTG 240  
Qy 318 GATGTTTTCCAGAGACCTTCCACAGGAGAAAGCCCTAGATAGCTTATCAGATGAC 377  
Db 241 GATGTTTTCCAGAGACCTTCCACAGGAGAAAGCCCTAGATAGCTTATCAGATGAC 300  
Qy 378 ACAGTATTAACCTGAATGTGCCCTTTAGAGTCACTTAAACAGCCCTTACTGCTGCG 437  
Db 301 ACAGTATTAACCTGAATGTGCCCTTTAGAGTCACTTAAACAGCCCTTACTGCTGCG 360  
Qy 438 ATTCATCCCGCAGTGGCCGAGTCTATACATTGAATTCACCCCTCCCAAACTGTGGGC 497  
Db 361 ATTCATCCCGCAGTGGCCGAGTCTATACATTGAATTCACCCCTCCCAAACTGTGGGC 420  
Qy 498 ATTCATGACCTGACCTGGGAGCCCTCTCATTACGCTGAGGATGATTAACAGAGACGTT 557  
Db 421 ATTCATGACCTGACCTGGGAGCCCTCTCATTACGCTGAGGATGATTAACAGAGACGTT 480  
Qy 558 ATCAAGAGACTAAAGGCTTATGAAGACCAACAGACAGTCTGATTTACAGAAA 617  
Db 481 ATCAAGAGACTAAAGGCTTATGAAGACCAACAGACAGTCTGATTTACAGAAA 540  
Qy 618 AAAGGGGTGCTGGAACATCTCCGGAACAGAAACCAAGATTTGGCCCTATGATAT 677  
Db 541 AAAGGGGTGCTGGAACATCTCCGGAACAGAAACCAAGATTTGGCCCTATGATAT 600  
Qy 678 GCTTTCCTACAAAGTAAAGTTCACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 737  
Db 601 GCTTTCCTACAAAGTAAAGTTCACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 659  
Qy 738 GAATGTGTACTATATATAGATGCGCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 797  
Db 660 GAATGTGTACTATATATAGATGCGCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 719  
Qy 798 TCGCTTT 804  
Db 720 TCGCTTT 726  
RESULT 13  
AAH06376  
ID AAH06376 standard; cDNA; 851 BP.  
XX  
AC AAH06376;  
XX  
DT 26-JUN-2001 (first entry)  
XX  
DE Human cDNA clone (5'-primer) SEQ ID NO:3211.  
XX  
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1074617-A2.  
XX  
PD 07-FEB-2001.  
XX  
PE 28-JUL-2000; 2000EP-0116126.  
XX  
PR 29-JUL-1999; 99JP-0248036.  
PR 27-AUG-1999; 99JP-0300253.  
PR 11-JAN-2000; 2000JP-0118776.  
PR 02-MAY-2000; 2000JP-0183767.  
PR 09-JUN-2000; 2000JP-0241899.  
XX  
PA (HELI-) HELIX RES INST.  
XX  
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;







```
Db 302 AAACATCATCCAGATGATGTGCATGACTCGGCTGGCCCTTCATGAGCTGAAAAATCTCACC 361
QY 300 CAGTATAGCTGGCTGTGGATGGTGTTCACAGACACTTCACAGGACAGAGCCCTAGAT 359
Db 362 CAGTATAGCTGGCTGTGGATGGTGTTCACAGACACTTCACAGGACAGAGCCCTAGAT 421
QY 360 AGAGCTTATCAGATCGACACAGATTAACCTGAATGTGCCCTTGAGTCAATTAAACAA 419
Db 422 AGAGCTTATCAGATCGACACAGATTAACCTGAATGTGCCCTTGAGTCAATTAAACAA 481
QY 420 CGCCTTACTGCTGCTGATTCATCCGCCAGTGGCCGAGTCTATAACATTGAATTCAAC 479
Db 482 CGCCTTACTGCTGCTGATTCATCCGCCAGTGGCCGAGTCTATAACATTGAATTCAAC 541
QY 480 CCTCCCAAAACTGTGGCATTGATGACCTGACTGGGGAGCCTCTCATTC-AGCGTGAGA 538
Db 542 CCTCCCAAAACTGTGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGA 601
QY 539 -TGATAACCGAGAGCGTTATCAAGAGACTAAAGCTTATGAAGCAACAAAGNCAG 597
Db 602 TTGATAAACGAGACGCTTATCAAGAGACTAAAGGCTTATGAAGCAACAAAGCCAG 661
QY 598 TCCTGNAFTATTACGAAAAAAGGGTGCTG 629
Db 662 TCCTGGGATATTACCAAGAAAAAAGGGGTG 693
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Search completed: March 19, 2003, 04:26:18  
Job time : 264 secs

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OM nucleic - nucleic search, using sw model

Run on: March 19, 2003, 03:11:20 : Search time 1475 Seconds  
(without alignments)  
9376.912 Million cell updates/sec

Title: US-10-006-190-2

Perfect score: 854  
Sequence: 1 GCCAGCCCAAGACCTGGT.....TGAATAATTATTACTTTA 854

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlmu:\*  
5: em\_estlov:\*  
6: em\_estlpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_hic:\*  
12: gb\_estl3:\*  
13: gb\_estl4:\*  
14: gb\_estl5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_fod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	832.6	97.5	1070	14	BM923355
2	797.4	93.4	979	14	BQ50443
3	699.2	81.9	1024	14	BQ050240
4	684.6	80.2	795	13	BQ050240
5	659.2	77.2	706	12	BG705248
6	659.2	77.2	851	9	AU130170

7	637.2	74.6	716	10	AV704895	AV704895
8	635.4	74.4	1183	12	BG106150	BG106150
9	633.8	74.2	924	14	BQ435142	BQ435142
10	623.8	73.3	833	13	B1553812	B1553812
11	605	70.8	902	12	BG619950	BG619950
12	595.2	69.7	639	9	AU126983	AU126983
13	594.2	69.6	716	10	AV695155	AV695155
14	581	68.0	711	12	BG687423	BG687423
15	578.6	67.8	803	9	AU136907	AU136907
16	573.4	67.1	1095	11	AK008681	AK008681
17	571.8	67.0	2758	11	AK004864	AK004864
18	571.8	67.0	2805	11	AK005194	AK005194
19	564.6	66.1	616	10	AV698046	AV698046
20	560.2	65.6	723	12	BG682861	BG682861
21	559	65.5	743	9	AL138385	AL138385
22	557.6	65.3	907	14	BQ714961	BQ714961
23	543	63.6	789	13	B1601992	B1601992
24	533.4	62.5	1110	13	B1415807	B1415807
25	529.2	62.0	616	10	AV707926	AV707926
26	528.4	61.9	705	12	BG698420	BG698420
27	526.2	61.6	870	13	B1257720	B1257720
28	523.6	61.3	626	14	BQ367213	BQ367213
29	511.4	59.9	802	13	B1601245	B1601245
30	508.2	59.5	1286	12	BG115825	BG115825
31	506.6	59.3	815	13	B1328500	B1328500
32	494.4	57.9	496	12	BF514669	BF514669
33	491.8	57.6	495	12	BF513711	BF513711
34	490	57.4	525	14	BQ270849	BQ270849
35	489.8	57.4	643	13	B8621249	B8621249
36	484.4	56.7	918	13	B1858992	B1858992
37	483	56.6	917	11	AK007618	AK007618
38	482.8	56.5	650	9	AI119333	AI119333
39	476.4	55.8	636	10	BB656931	BB656931
40	474.8	55.6	515	9	AA007279	AA007279
41	471.8	55.2	1137	13	BM478239	BM478239
42	471.2	55.2	522	13	BM272857	BM272857
43	471.2	55.2	600	14	BM837013	BM837013
44	469.6	55.0	700	13	B1561819	B1561819
45	465	54.4	677	14	BQ694111	BQ694111

#### ALIGNMENTS

RESULT 1  
LOCUS BM923355 1070 bp mRNA linear EST 12-MAR-2002  
DEFINITION AGENCOURT\_6625937 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5758957  
5', mRNA sequence.  
ACCESSION BM923355  
VERSION BM923355.1 GI:19373734  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1070)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapds-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: L1AM12803 row: j column: 14  
High quality sequence stop: 686.  
Location/Qualifiers  
1. 1070

FEATURES  
source



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 QY 240 AACATCATCCAGATGATGTCATGACTGGCTGCTTCATGAGTGAATAATCTCACC 239  
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 Db 325 AACATCATCCAGATGATGTCATGACTGGCTGCTTCATGAGTGAATAATCTCACC 384  
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 QY 660 ATTTGGCCCTATGATATGCTTTCCTCAAAAGTTCACAAAGCCAGAAAGCT 719  
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 Db 744 ATTTGGCCCTATGATATGCTTTCCTCAAAAGTTCACAAAGCCAGAAAGCT 803  
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 QY 720 TCAGTTACTGATGAGAGAAATGTTGTACTATTTAATGTAAGATGGGCAAAAGCT 779  
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 Db 804 TCAGTTACTGATGAGAGAAATGTTGTACTATTTAATGTAAGATGGGCAAAAGCT 863  
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 QY 780 AGTCCTGATTTAGAGAGCTGCTTTCCTAAGACTTCTAGTATGAA-TCCTTGA 838  
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 Db 864 AGTCCTGATTTAGAGAGCTGCTTTCCTAAGACTTCTAGTATGAA-TCCTTGA 923  
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 QY 839 AATTATATTTACTTT 852  
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 Db 924 AATTATATTTACTTT 937  
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**RESULT 3**  
 B0050240 1024 bp mRNA linear EST 29-MAR-2002  
 LOCUS AGENCOUPT\_7050937 NIH\_MGC\_71 Homo sapiens cDNA clone IMAGE:5784135  
 DEFINITION 5', mRNA sequence.  
 ACCESSION B0050240  
 VERSION B0050240.1 GI:19809580  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1024)  
 AUTHORS NIH-MGC http://mgi.ncl.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: c9abbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 plate: LNL12869 row: C column: 16  
 high quality sequence stop: 539.  
 Location/Qualifiers  
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 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: uterus; Vector: pCMV-Sport6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 2.1 kb."

BASE COUNT 302 a 251 c 240 g 231 t  
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 Query Match 81.9%; Score 699.2; DB 14; Length 1024;  
 best Local Similarity 95.7%; Pred. No. 7.8e-188;  
 Matches 760; Conservative 0; Mismatches 30; Indels 4; Gaps 4;

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 Db 1 CATGGGGGCGTCGCGCGCTGCTGCGAGCGGTGATGAGGGCCCGGGCTGCGGCAA 60  
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 QY 110 GGGCACCCTGTCGTGCGGCATCACTACACACTTGCAGCTGAAGCCTTCCAGCGGGA 169  
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 Db 61 GGGCACCCTGTCGTGCGGCATCACTACACACTTGCAGCTGAAGCCTTCCAGCGGGA 120  
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 QY 170 CTTGCTCCGGGACAAACATGCTGCGGGGACAGAAATTTGGCTGTAGCCAAAGCTTTCAT 229  
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 Db 121 CTTGCTCCGGGACAAACATGCTGCGGGGACAGAAATTTGGCTGTAGCCAAAGCTTTCAT 180  
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 QY 230 TGAACCAAGGAAACTCATCCAGATGATGATGATGCTGCGTGGCCCTTCATGAGTGA 289  
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 Db 181 TGAACCAAGGAAACTCATCCAGATGATGATGATGATGATGATGATGATGATGATGAT 240  
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 Db 241 AATCTCACCAGTATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
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 QY 350 AGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 409  
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 Db 301 AGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
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 Db 361 CATTAAACAGCGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
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 Db 421 TGAATTAACCCCTCCAAAACGTGGGCATTTGATGATGATGATGATGATGATGATGATGAT 480  
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 QY 530 GCGTGAAGATGATTAACACAGAGAGCTTATCAAGAGACTTAAGCTTATGAAGCCAAAG 589  
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 Db 481 GCGTGAAGATGATTAACACAGAGAGCTTATCAAGAGACTTAAGCTTATGAAGCCAAAG 540  
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 Db 541 AAAGCCAGTCTGAGNTATTTACAGAAAAAAGGGGTGCTGAAACATTCCTCCGGAAC 600  
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 QY 647 AGAACCACAAAGATTTGGCCCTATGATGATGATGATGATGATGATGATGATGATGATGAT 706  
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 Db 601 AGAACCACAAAGATTTGGCCCTATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
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 QY 707 AAGCCAAAGCTTCACTTCACTGATGAGGAGAAATGTTGTTATGATGATGATGATGATGATGAT 766  
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 Db 661 AAGCCAAAGCTTCACTTCACTGATGAGGAGAAATGTTGTTATGATGATGATGATGATGATGAT 719  
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 QY 767 GGGCAAACTCTAGTCTTTCATTTAGAAAGCTGCTTTCCTAAGACTTCTAGATGATGAT 826  
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 Db 720 GGGCAAACTCTAGTCTTTCATTTAGAAAGCTGCTTTCCTAAGACTTCTAAGAGAT 779  
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QY	827	GAATCTTTGA	840
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Db	780	GGATTCTTGCAA	793
RESULT 4			
LOCUS	B1550730		
DEFINITION	60319561F1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:5274916 5',	795 bp	mRNA linear EST 05-SEP-2001
VERSION	B1550730		
KEYWORDS	B1550730.1 GI:15438042		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/.		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: Marios Palkovits, M.D., Ph.D.		
	CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shireki		
	Toshiyuki and Piero Carninci (RIKEN)		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLN at:		
	http://image.lnl.gov		
	Plate: L16M1694 row: b column: 05		
	High quality sequence stop: 763.		
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	/clone_lib="NIH_MGC_95"		
	/tissue_type="hippocampus"		
	/lab_host="DH10B"		
	/note="Organ: brain; Vector: Bluescript (modified		
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	); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',		
	size-selected for average insert size 2.5 kb and		
	normalized to R0F 5. This is a primary library enriched		
	for full-length clones and constructed using the		
	Cap-trapper method (Carninci, in preparation). Library		
	constructed by M. Brownstein (NIH/NHGRI, National		
	Institutes of Health). Note: this is a NIH-MGC Library."		
BASE COUNT	207 a 208 c 220 g 160 t		
ORIGIN			
Query Match	80.2%; Score 684.6; DB 13; Length 795;		
Best Local Similarity	97.8%; Pred. No. 1e-183;		
Matches 745; Conservative	0; Mismatches 12; Indels 5; Gaps 5;		
QY	1	GCCANAGCCCAAGCCCTGTACCCGCGGGG-GGGCCCTCAGTCTGGGCGCATGGGGGCG	59
Db	23	GGCCAGGCCCAAGCCCTGTACCCGCGGGGCTTCAGTCTGGGCGCATGGGGGCG	82
QY	60	TCCGCGGGGCTGTGCGAGCGGTATCATGGGGGCCCCGCGGCTCGGGGCAAGGCAACCGTG	119
Db	83	TCCGCGGGGCTGTGCGAGCGGTATCATGGGGGCCCCGCGGCTCGGGGCAAGGCAACCGTG	142
QY	120	TCTGTGCGGCACTACACACTTTCAGAGCTGAAGCACTCTCCAGCGGGGACCTGCTCCGG	179
Db	143	TCTGTGCGGCACTACACACTTTCAGAGCTGAAGCACTCTCCAGCGGGGACCTGCTCCGG	202
QY	180	GACAAACATGCTGCGGGGCAAGAAATTTGGCTGTAGCAAGGCTTTCATTGACCAAGG	239
Db	203	GACAAACATGCTGCGGGGCAAGAAATTTGGCTGTAGCAAGGCTTTCATTGACCAAGG	262

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
OY 240	AAACGATCCCGAGATGATCATGCTCGGGGCGCCCTTCATGAGCTGAAAAATCTCAC	BG705248	602687928F1	NIH_MGC_95 Homo sapiens CDNA clone IMAGE:4820383 5 ,	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
Db 263	AAACTCATCCAGATGATGTCATGCTGCTGGCCCTTCATGAGCTGAAAAATCTCAC	BG705248	BG705248.1	GI:13979395	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
OY 300	CAGATATACCTGGCTGGTGGATGGTTTTCCAAAGACACTTCCACAGCAGAAAGCCCTAGAT	BG705248	602687928F1	NIH_MGC_95 Homo sapiens CDNA clone IMAGE:4820383 5 ,	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
Db 323	CAGATATACCTGGCTGGTGGATGGTTTTCCAAAGACACTTCCACAGCAGAAAGCCCTAGAT	BG705248	BG705248.1	GI:13979395	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
OY 360	AGAGCTTATCAGATTCGACACAGTGTATTAACCTGATATGCCCCCTTGAGGTGATTTAAACA	BG705248	602687928F1	NIH_MGC_95 Homo sapiens CDNA clone IMAGE:4820383 5 ,	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
Db 383	AGAGCTTATCAGATTCGACACAGTGTATTAACCTGATATGCCCCCTTGAGGTGATTTAAACA	BG705248	BG705248.1	GI:13979395	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
OY 420	CGCCTTACTGCTCGCTGGATTCATCCGCCAGATGCGCCAGTCTATTAAGATTGAATTCAC	BG705248	602687928F1	NIH_MGC_95 Homo sapiens CDNA clone IMAGE:4820383 5 ,	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
Db 443	CGCCTTACTGCTCGCTGGATTCATCCGCCAGATGCGCCAGTCTATTAAGATTGAATTCAC	BG705248	BG705248.1	GI:13979395	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
OY 480	CCTCCCAAAAGCTGTGGGCAATGATGACCTGACTGSGGAGCCCTTCATTCAGCGTAGAT	BG705248	602687928F1	NIH_MGC_95 Homo sapiens CDNA clone IMAGE:4820383 5 ,	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
Db 503	CCTCCCAAAAGCTGTGGGCAATGATGACCTGACTGSGGAGCCCTTCATTCAGCGTAGAT	BG705248	BG705248.1	GI:13979395	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
OY 540	GATTAACCAAGAGCGGTATCAAGAGACTTAAAGGTTTATGAAGACCAAAAGACAGTC	BG705248	602687928F1	NIH_MGC_95 Homo sapiens CDNA clone IMAGE:4820383 5 ,	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
Db 563	GATTAACCAAGAGCGGTATCAAGAGACTTAAAGGTTTATGAAGACCAAAAGACAGTC	BG705248	BG705248.1	GI:13979395	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
OY 600	CTGGATATTTATCCAGA -AAAAAGGGGTCTGGAACATTTCTCCGAGACAGAAACCAACA	BG705248	602687928F1	NIH_MGC_95 Homo sapiens CDNA clone IMAGE:4820383 5 ,	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
Db 623	CTGGATATTTATCCAGA -AAAAAGGGGTCTGGAACATTTCTCCGAGACAGAAACCAACA	BG705248	BG705248.1	GI:13979395	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
OY 659	GATTTGGCCCTATGATATATGCTTCTTCACAACTAAAGTCTCCACAAAGACCCAG -AAG	BG705248	602687928F1	NIH_MGC_95 Homo sapiens CDNA clone IMAGE:4820383 5 ,	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 706)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
Db 683	GATTTGGCCCTATGATATATGCTTCTTCACAACTAAAGTCTCCACAAAGACCCAG -AAG	BG705248	BG705248.1	GI:13979395	human.	Homo sapiens	Eukaryota; Met				





Db 570 CCTCCCAAAACGTGTGGCATGTGATGACCTGCTGGGAGCCCTCTCATTCAGCGTGAGAT 629  
QY 540 GATAAACGAGAGCGGTTATCAAGAGACTAAAGGCTTATGAAACCAAAACAGNAGTC 599  
Db 630 GATTAACCGAGAGCGGTTATCAAGAGACTAAAGGCTTATGAAACCAAAACAGNAGTC 669  
QY 600 CTGGNATATTACAGAAAAAGGGGCTGTGAAACATCTCCGGAACAGAACCAACAG 659  
Db 690 CTGGAATATTACAGAAAAAGGGGCTGTGAAACATCTCTCGG-ACAGAAACCAACAG 748  
QY 660 ATTGGCCCTATGATATGCTTCTTCTACAAACTAAAGTTCCAGAAAGCCGAAAGCT 719  
Db 749 ATTGG-CCTAGNATATCTTTCTTCTACAAAGTTCCAGAAAGCCGAAAGCT 807  
QY 720 TCAGTACTCATGAGAG-AAAATGTGTGTAATTAAT 758  
Db 808 TTAGTACTTCATGAGAGAAATGTGTGTAATTAAT 850

RESULT 7  
AV704895 716 bp mRNA linear EST 09-OCT-2000  
LOCUS AV704895 ADB Homo sapiens cDNA clone ADBXH03 5', mRNA sequence.  
DEFINITION AV704895  
VERSION AV704895.1 GI:10722206  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 716)  
AUTHORS Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao  
H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z.,  
Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu  
G., Hu, R., Chen, J., Chen, Z., and Han, Z.  
Homo sapiens cDNA ADB clones  
Unpublished (2000)  
CONTACT: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203 P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.

FEATURES  
source location/Qualifiers  
1..716  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="ADBXH03"  
/clone\_1ib="ADB"  
/tissue\_type="Adrenal gland"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 210 a 168 c 161 g 171 t 6 others

ORIGIN  
Query Match 74.6%; Score 637.2; DB 10; Length 716;  
Best Local Similarity 96.4%; Pred. No. 36-170;  
Matches 690; Conservative 0; Mismatches 21; Indels 5; Gaps 4;

QY 126 CGCATCATACACACTTTCAGCTGAAGACCTCCAGGGGAGACCTGCGGGGACAC 185  
Db 1 CGCATCATACACACTTTCAGCTGAAGACCTCCAGGGGAGACCTGCGGGGACAC 60

QY 186 ATGCTGCGGGGACAGAAATTTGGCGTTAGCCAAAGCTTTATGACCAAGGAAGTAC 245  
Db 61 ATGCTGCGGGGACAGAAATTTGGCGTTAGCCAAAGCTTTATGACCAAGGAAGTAC 120

QY 246 ATCCCAAGATGATGATGACTGCGGCTGCGCTTCATGAGCTGAAAAATTCACCCAGTAT 305  
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Db 121 ATCCAGATGATGATGATGACTGCGGCTGCGCTTCATGAGCTGAAAAATTCACCCAGTAT 180  
QY 306 AGCTGCTGTGGATGGTTTTCCAGAGACCTCCAGGGCAGAACCCAGATTAAGCT 365  
Db 181 AGCTGCTGTGGATGGTTTTCCAGAGACCTTCACAGGACAGAACCCAGATTAAGCT 240  
QY 366 TATCAGATGACACAGTGAATTAACCTGAATGTCCTTTGAGGTCATTTAAACACCTTT 425  
Db 241 TATCAGATGACACAGTGAATTAACCTGAATGTCCTTTGAGGTCATTTAAACAGCTTT 300  
QY 426 ACTGCTGCTGATTCATCCCGCACTGCGCCAGTGTATTAACATTTAAACCTCC 485  
Db 301 ACTGCTGCTGATTCATCCCGCACTGCGCCAGTGTATTAACATTTAAACCTCC 360  
QY 486 AAACAGTGGGCTTATGATGACCTGAGGAGCCCTCATTCAGGTGAGTGAATTA 545  
Db 361 AAACAGTGGGCTTATGATGACCTGAGGAGCCCTCATTCAGGTGAGTGAATTA 420  
QY 546 CCAGAGACGTTTATCAAGAGACTAAAGGCTTATGAAGACCAACAAAGNAGCTCGNA 605  
Db 421 CCAGAGACGTTTATCAAGAGACTAAAGGCTTATGAAGACCAACAAAGNAGCTCGNA 480  
QY 606 TATTACCAGAAAAAGGGGCTGTGAACATTCCTCGGAACAGAAACCAAGATTTGG 665  
Db 481 TATTACCAGAAAAAGGGGCTGTGAACATTCCTCGGAACAGAAACCAAGATTTGG 540  
QY 666 CCTATGATATGCTTCTTCTACAAACTAAAGTCCCAAG--AAGCCAAAGCTTCAG 723  
Db 541 CCTATGATATGCTTCTTCTACAAACTAAAGTCCCAAGGAAAGCAAGAAAGCTTCAG 600  
QY 724 TTTACTCATGAGG-AGAAATGTGTAA-CTATTATAGTAGAGTGGCAACCTCTGAG 781  
Db 601 NTACTTCATGAGAAAGAAATGTGTGTATACCTATTATAGTAGAGTGGCAACCTCTGAG 660  
QY 782 TCTTGCATTTAGAGCTGCTTCT-AGAGCTTGTAGTAGATGAATTCCTTG 836  
Db 661 GCCTTGTCTTGAAGCTGCTTCTTCTAAAGACTCTAGATGATGAATTCCTTG 716

RESULT 8  
BG106150 1183 bp mRNA linear EST 30-JAN-2001  
LOCUS BG106150  
DEFINITION 602289978F1 NIH\_MGC\_85 Homo sapiens cDNA clone IMAGE:4385034 5',  
mRNA sequence.  
ACCESSION BG106150  
VERSION BG106150.1 GI:12599996  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 1183)  
AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
COMMENT Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Louis Staudt, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LHAM10065 row: k column: 19  
High quality sequence stop: 683.

FEATURES  
source location/Qualifiers  
1..1183  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4385034"  
/clone\_1ib="NIH\_MGC\_85"  
/tissue\_type="Lymphoma, cell line"

/lab\_host="DH10B (phage-resistant)"  
/note="Organ: Lymph; Vector: PCMV-SPOrt6; Site:1: NotI;  
Site:2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.867 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH-MGC Library."

BASE COUNT 345 a 273 c 334 g 231 t  
ORIGIN

Query Match 74.4%; Score 635.4; DB 12; Length 1183;  
Best Local Similarity 94.3%; Pred. No. 1.2e-169;  
Matches 679; Conservative 0; Mismatches 39; Indels 2; Gaps 2;

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QY 1 GCCANGCCCAAGCCCTGATACCGCGCGGCTG-GGGCTCAGTCTGCGGCATGCGGGCG 59
D 6 GCGCAGGCGCCAAAGCCCTGATACCGCGCGGCTGCGGCCTCAGTCTGCGGCATGCGGGCG 65
QY 60 TCCGCGCGGCTGCTGCGAGCGGTGATCATGGGGCCCGGCGCTCGGCAAGGCGACCGTG 119
D 66 TCCGCGCGGCTGCTGCGAGCGGTGATCATGGGGCCCGGCGCTCGGCAAGGCGACCGTG 125
QY 120 TCGTCGGGCTACACTACACCTTCGAGCTAAGCAGCTCTTCAGCGGGGACCTGCTCCG 179
D 126 TCGTCGGGCTACACTACACCTTCGAGCTAAGCAGCTCTTCAGCGGGGACCTGCTCCG 185
QY 180 GACAACATGCTGGGGGCGACAGAAATGGCGTGTAGCAAGGCTTCATTTGACACAGG 239
D 186 GACAACATGCTGGGGGCGACAGAAATGGCGTGTAGCAAGGCTTCATTTGACACAGG 245
QY 240 AAATCATCCCAAGATGATGTCATGCTGCGCTGCGCTTCATGAGCTGAAATCTCACC 299
D 246 AAATCATCCCAAGATGATGTCATGCTGCGCTGCGCTTCATGAGCTGAAATCTCACC 305
QY 300 CAGTATAGCTGGCTGTTGGATGGTTTCCAAAGACACTTCCACAGCGCAAGCCCTGAT 359
D 306 CAGTATAGCTGGCTGTTGGATGGTTTCCAAAGACACTTCCACAGCGCAAGCCCTGAT 365
QY 360 AGAGCTTATCAGATCGACAGATGATTAACCTGAATGTCCTTGAAGCATTAACAA 419
D 366 AGAGCTTATCAGATCGACAGATGATTAACCTGAATGTCCTTGAAGCATTAACAA 425
QY 420 CGCCTTACTGCTGCTGGATTCATCCGCGCAGTGGCGGAGTCTATAACATTTGAATTC 479
D 426 CGCCTTACTGCTGCTGGATTCATCCGCGCAGTGGCGGAGTCTATAACATTTGAATTC 485
QY 480 CCTCCCAAACTGTGGCATTTGATGACCTGCTGAGGAGGCTCTCATTTACGCTGAGAT 539
D 486 CCTCCCAAACTGTGGCATTTGATGACCTGCTGAGGAGGCTCTCATTTACGCTGAGAT 545
QY 540 GATTAACAGAGAGGTTTATCAAGAGACTAAAGGCTTATGAAGCC-AAACAAAGNAGT 598
D 546 GATTAACAGAGAGGTTTATCAAGAGACTAAAGGCTTATGAAGCC-AAACAAAGNAGT 605
QY 599 CCTGNAATATTACAGAAAAAGGGGTCTGAAACATTTCTCGGAGACAGAAACCAAA 658
D 606 CCTGNAATATTACAGAAAAAGGGGTCTGAAACATTTCTCGGAGACAGAAACCAAA 665
QY 659 GATTGGCCCTATGATATGCTTTCTTCAAACTAAAGTTCACAAAGAACAGAGAGG 718
D 666 GATTGGCCCTATGATATGCTTTCTTCAAACTAAAGTTCACAAAGAACAGAGAGG 725

RESULT 9
BQ435142
LOCUS BQ435142 924 bp mRNA linear EST 24-MAY-2002
DEFINITION AGENCOURT_7914060 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6156916
5', mRNA sequence.
ACCESSION BQ435142
VERSION BQ435142.1 GI:21174218
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

REFERENCE  
1 (bases 1 to 924)  
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9abs-r@mail.nih.gov  
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>

Plate: LLM13501 row: p column: 05  
High quality sequence start: 225  
High quality sequence stop: 379.  
Location/Qualifiers

## FEATURES

source  
1. 924  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="IMAGE:6156916"  
/clone\_lib="NIH\_MGC\_71"  
/tissue\_type="leiomysarcoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: uterus; Vector: PCMV-SPOrt6; Site:1: NotI;  
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2.1 kb."  
BASE COUNT 280 a 191 c 213 g 239 t 1 others  
ORIGIN

Query Match 74.2%; Score 633.8; DB 14; Length 924;  
Best Local Similarity 97.9%; Pred. No. 3.1e-169;  
Matches 641; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 200 AGAATTTGGCGTGTATGACCAAGGCTTTCATTTGACCAAGGCAAACTCCAGATGATGT 259
D 31 AGAATTTGGCGTGTATGACCAAGGCTTTCATTTGACCAAGGCAAACTCCAGATGATGT 90
QY 260 CAGTACTGCGCTGCGCTTCATGAGCTGAAAATCTCACCAGATAGCTGGCTGGGA 319
D 91 CAGTACTGCGCTGCGCTTCATGAGCTGAAAATCTCACCAGATAGCTGGCTGGGA 150
QY 320 TCGTTTCCAAAGACACTTCCACAGCGAAGCCCTGATAGACTTATCAGATCGACAC 379
D 151 TCGTTTCCAAAGACACTTCCACAGCGAAGCCCTGATAGACTTATCAGATCGACAC 210
QY 380 AGTGAATTAACCTGAATGTCCTTTGAGGTCAATTAACCAACGCTTACTGCTGCTGAT 439
D 211 AGTGAATTAACCTGAATGTCCTTTGAGGTCAATTAACCAACGCTTACTGCTGCTGAT 270
QY 440 TCATCCGCGCAGTGGCGGAGTCTTAACATTTGAATTCACCTCCAAACTGGGGCAT 499
D 271 TCATCCGCGCAGTGGCGGAGTCTTAACATTTGAATTCACCTCCAAACTGGGGCAT 330
QY 500 TGATGACCTGACTGCGGAGGCTCTCATTTACAGCGTGAAGATGATTAACCAAGAGGTTAT 559
D 331 TGATGACCTGACTGCGGAGGCTCTCATTTACAGCGTGAAGATGATTAACCAAGAGGTTAT 390
QY 560 CAAGAGACTAAAGGCTTATGAAGACCAAAACAGNCAGTCTGATATTATTCAGAAAAA 619
D 391 CAAGAGACTAAAGGCTTATGAAGACCAAAACAGNCAGTCTGATATTATTCAGAAAAA 450
QY 620 AGGGGTGCTGGAAACATTTCCGGAAGAAACCAACAGATTTGGCCCTATGATATGC 679
D 451 AGGGGTGCTGGAAACATTTCCGGAAGAAACCAACAGATTTGGCCCTATGATATGC 510
QY 680 TTTCTTCAAACTTAAAGTTTCACAAAGAGCGCAAAAGCTTCACTTACTCATAGAGAGA 739
D 511 TTTCTTCAAACTTAAAGTTTCACAAAGAGCGCAAAAGCTTCACTTACTCATAGAGAGA 570
QY 740 AATGTGTAACTTATATAGTAAAGATGGGCAACCTCTAGTCTTCATTTGAAGCT 799
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Db      571 AATGCTGGAAGTATTATAGTAGATGGCAAACTCCTAGTCTTGATTTAGAGCT 630
QY      800 GCTTTCCTAGACTCTAGTATGTATGAATCTTTGAAAATATATCTTTTA 854
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      631 GCTTTTCTAAGACTCTAGTATGATGATGATTTTGAATAATCATATTTACTTTTA 685

RESULT 10
BI553912          833 bp  mRNA      linear  EST 05-sep-2001
LOCUS             BI553912
DEFINITION       603190877F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:526206 5',
                mRNA sequence.
ACCESSION        BI553912
VERSION          BI553912.1 GI:15441224
KEYWORDS         EST.
SOURCE           human.
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE        1 (bases 1 to 833)
AUTHORS          NIH-MGC http://mgi.ncl.nih.gov/.
TITLE            National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL          Unpublished (1999)
COMMENT          Contact: Robert Strausberg, Ph.D.
                  Email: cgapbs-remail.nih.gov
                  Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
                  cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
                  Toshitaki and Piero Carninci (RIKEN)
                  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                  DNA Sequencing by: Incyte Genomics, Inc.
                  Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LLNL at:
                  http://image.llnl.gov
                  Plate: LLM11660 row: j column: 19
                  High quality sequence stop: 801.

FEATURES
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    /db_xref="taxon:9606"
    /clone_1b="NIH_MGC_95"
    /clone_1lb="NIH_MGC_95"
    /tissue_type="hippocampus"
    /lab_host="DH10B"
    /note="Organ: Brain; Vector: pBluescriptR (modified
    Bluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
    ); Oligo-dT primed using primer 5'-TTTCTTTTCTTTTCTTCTT-3',
    size-selected for average insert size 2.5 kb and
    normalized to 10^5. This is a primary library enriched
    for full-length clones and constructed using the
    Cap-trapper method (Carninci, in preparation). Library
    constructed by M. Brownstein (NHGRI/NHGRI, National
    Institutes of Health). Note: this is a NIH-MGC Library."
BASE COUNT      207 a      230 c      233 g      163 t
ORIGIN
Query Match      73.3%; Score 625.8; DB 13; Length 833;
Best Local Similarity 95.9%; Pred. No. 5,6e-167;
Matches 683; Conservative 0; Mismatches 25; Indels 4; Gaps 4;
QY      1 GCCANCCCAAGCCCTGTACCCCGCGTG-GGGCTTCATCTGCGCCATGGGGCG 59
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      95 GGCAGAGCCAAAGCCCTGTACCCCGCGTGCGGCCCTCACTGCGGCATGGGGCG 154
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      60 TCCGCGCGCTCTGCGAGCGGTGATCATGGGGCCCGGCTCGGCAAGGCAACCGTG 119
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      155 TCCGCGCGCTCTGCGAGCGGTGATCATGGGGCCCGGCTCGGCAAGGCAACCGTG 214
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      120 TCGTCGCGCATCACTACACTTTCAGCTGAAGCAACCTCTCCAGCGGGACCTGCTCCG 179
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      215 TCGTCGCGCATCACTACACTTTCAGCTGAAGCAACCTCTCCAGCGGGACCTGCTCCG 274
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      180 GACACATCTCTCGGGGCAACAAATTGGCGTTTACCAAGCCTTTTACCAAGG 239
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db      275 GACACATCTCTCGGGGCAACAAATTGGCGTTTACCAAGCCTTTTACCAAGG 334
QY      240 AACATCATCCGATGATGATCAATGAGTGGCGCCCTTCATGAGCTGAAAATCTCAC 299
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      335 AACATCATCCGATGATGATGATGATGAGTGGCGCCCTTCATGAGCTGAAAATCTCAC 394
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      300 CAGTATAGCTGCGCTTGGATGCTTTTCCAGAGACACTTCCACAGGCAAGCCCTAGAT 359
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Db      395 CAGTATAGCTGCGCTTGGATGCTTTTCCAGAGACACTTCCACAGGCAAGCCCTAGAT 454
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      360 AGAGCTTATCAGATGACACAGTATTAACCTGATGTGCCCTTTGAGGTCTTAACAA 419
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      455 AGAGCTTATCAGATGACACAGTATTAACCTGATGTGCCCTTTGAGGTCTTAACAA 514
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      420 CGCTTACTGCTGCGGTGATTCATCCCGCAGTGGCCGCGAGTCAATTAATTAAC 479
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      515 CGCTTACTGCTGCGGTGATTCATCCCGCAGTGGCCGCGAGTCAATTAATTAAC 574
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      480 CCTCCCAAACTGTGGGCAATGATGACCTGAGTGGGAGCCCTCTCATTCAGCGTGAAGAT 539
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Db      575 CCTCCCAAACTGTGGGCAATGATGACCTGAGTGGGAGCCCTCTCATTCAGCGTGAAGAT 634
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QY      540 GATTAACCGAGACGCTTATCAAGAGAC-TAAAGCTTATGAAGA-CCAAACAAAGNCAG 597
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Db      635 GATTAACCGAGACGCTTATCAAGAGACTTAAAGGCTTATGAAGACCCAAACAAAGCCAG 694
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QY      598 TCGTGTATATTAACAG-AAAAAGGGGCTGGAAGCTTCCGGAACAGAAACCAAC 656
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Db      695 TCGTGTATATTAACAGAAAAAGGGGCTGGAAGCTTCCGGAACAGAAACCAAC 754
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QY      657 AAGATTGGCCCTATGATATGCTTTCCTACAAGCTAAAGTTCCACAAAGAA 708
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Db      755 AAGATTGGCCCTATGATATGCTTTCCTACAAGCTAAAGTTCCACAAAGAA 806
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RESULT 11
BI619950          902 bp  mRNA      linear  EST 18-Apr-2001
LOCUS             BI619950
DEFINITION       602618148F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4731898 5',
                mRNA sequence.
ACCESSION        BI619950
VERSION          BI619950.1 GI:13671321
KEYWORDS         EST.
SOURCE           human.
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE        1 (bases 1 to 902)
AUTHORS          NIH-MGC http://mgi.ncl.nih.gov/.
TITLE            National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL          Unpublished (1999)
COMMENT          Contact: Robert Strausberg, Ph.D.
                  Email: cgapbs-remail.nih.gov
                  Tissue Procurement: CLONTECH Laboratories, Inc.
                  cDNA Library Preparation: CLONTECH Laboratories, Inc.
                  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                  DNA Sequencing by: Incyte Genomics, Inc.
                  Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LLNL at:
                  http://image.llnl.gov
                  Plate: LLM1590 row: p column: 11
                  High quality sequence stop: 772.

FEATURES
    source         location/Qualifiers
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    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_1b="NIH_MGC_79"
    /clone_1lb="NIH_MGC_79"
    /lab_host="DH10B (TI phage-resistant)"
    /note="Organ: placenta; Vector: pDNR-LIB (Clontech);
    Site_1: SfiI (ggccgctcgagc); Site_2: SfiI (ggccatgatgac
    ); 5' and 3' adaptors were used in cloning as follows: 5'
    adaptor sequence: 5'-CACGGCCATTATGACC-3' and 3' adaptor

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sequence: 5'-ATTCTAGAGCCGAGCGCGGACATG-dt(30)BN-3'  
(where B = A, C, G, or T). Average  
insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA). Note: this is a NIH-MGC  
Library."

BASE COUNT 275 a 199 c 181 g 247 t  
ORIGIN

## Query Match

70.8%; Score 605; DB 12; Length 902;

Best Local Similarity 99.2%; Pred. No. 4.8e-161;

Matches 638; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

OY 215 AGCGAAGGCTTTCATGACCAAGGAAACCATCCAGATGATGCTGCTGGCTGGC 274  
|||||  
Db 1 AGCGAAGGCTTTCATGACCAAGGAAACCATCCAGATGATGCTGCTGGCTGGC 60  
OY 275 CCTTCATGAGCTGAAATCTCACCAGTATAGCTGGCTGGTGGATTTTCCAAGAC 334  
|||||  
Db 61 CCTTCATGAGCTGAAATCTCACCAGTATAGCTGGCTGGTGGATTTTCCAAGAC 120  
OY 335 ACTTCCACAGGACGAAACCCCTAGATAGAGCTTATCAGATGACACAGTGAATTAACCTGAA 394  
|||||  
Db 121 ACTTCCACAGGACGAAACCCCTAGATAGAGCTTATCAGATGACACAGTGAATTAACCTGAA 180  
OY 395 TGTGCCCCCTTGAAGCTATTAAACAAGCCCTTACTGCTGGATTCATCCCGCAGTGG 454  
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Db 181 TGTGCCCCCTTGAAGCTATTAAACAAGCCCTTACTGCTGGATTCATCCCGCAGTGG 240  
OY 455 CCGAGCTATTAACATTGAATTCACCCCTCCCAAACTGTGGGATGATGACCTGACCTGG 514  
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Db 241 CCGAGCTATTAACATTGAATTCACCCCTCCCAAACTGTGGGATGATGACCTGACCTGG 300  
OY 515 GGAGCCTCTCATTCACGCTGAGAGATATAAACGAGACGCTTATCAAGAGACTAAAGGC 574  
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Db 301 GGAGCCTCTCATTCACGCTGAGAGATATAAACGAGAGCGTATATCAAGAGACTAAAGGC 360  
OY 575 TTATGAAGACCAACAAGCAGTCTCGATATTACAG-AAAAAGGGGCTGTGAAA 633  
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Db 361 TTATGAAGACCAACAAGCAGTCTCGATATTACCAAAAAAGGGGCTGTGAAA 420  
OY 634 CATTCCTCGGAACAGAACCAAGATTGGCCCTATGTATATGCTTCTCAAACTA 693  
|||||  
Db 421 CATTCCTCGGAACAGAACCAAGATTGGCCCTATGTATATGCTTCTCAAACTA 480  
OY 694 AAGTTCACAGAAAGCCAGAAAGCTTCAGTACTCCATGAGAGAA- TGTGTGTAA-C 751  
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Db 481 AAGTTCACAGAAAGCCAGAAAGCTTCAGTACTCCATGAGAGAAAGTGTGTAAAC 540  
OY 752 TATTATAGTAAGATGGGCAACCTCTAGTCTCTGCAATTAGAAGCTGCTTTTCTTAAG 811  
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Db 601 ACTTCTAGTATGATGAATCTTTGAATAATTATTACTTTTA 643

RESULT 12  
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LOCUS AUI26983  
DEFINITION AUI26983 NT2RP2 Homo sapiens cDNA clone NT2RP2000329 5', mRNA  
sequence.  
ACCESSION AUI26983  
VERSION AUI26983.1 GI:10951699  
KEYWORDS  
SOURCE  
ORGANISM human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 639)  
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,

TITLE Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and  
Isogai,T.  
JOURNAL HRI human CDNA project  
COMMENT Unpublished (2000)  
Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-33975  
Fax: 81-438-52-33986  
Email: genomics@hri.co.jp  
HRI human CDNA project; 5'- & 3'-end one pass sequencing; Helix  
Research Institute; cDNA library construction; Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.

## FEATURES

## source

1. 639  
/organism="Homo sapiens"  
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/clone\_1ib="NT2RP2"  
/cell\_type="teratocarcinoma"  
/cell\_line="NT2"  
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor  
cells after 2-weeks retinoic acid (RA) induction"

BASE COUNT 170 a 167 c 155 g 138 t 9 others  
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## Query Match

69.7%; Score 595.2; DB 9; Length 639;

Best Local Similarity 96.1%; Pred. No. 2.6e-158;

Matches 614; Conservative 0; Mismatches 24; Indels 1; Gaps 1;

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OY 97 CGGGCTCGGGCAAGGCGACGCTGCGCGGCACTACACTGACACTGAGAGAC 156  
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OY 157 TCTCCAGCGGGGACCTGCTCCGGGACAACTGCTGCGGGGACAGAAATTTGGCGTGTAG 216  
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Db 181 CCAAGCTTTCATTTAGACCAAGGAACTCATCCAGATGATGATGATGATGATGATG 240  
OY 277 TTGATGAGCTGAAAAATCTGACCCAGATATGAGCTGGGCTGTGGATGGTTTCCAAGGAC 336  
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ACCESSION AV695155
VERSION   AV695155.1 GI:10297018
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 716)
AUTHORS   Xu,X., Huang,J., Yu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Ou,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z., and Han,Z.
TITLE     Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE   21625106
COMMENT   Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

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Best Local Similarity 98.4%; Pred. No. 5.2e-158;
Matches 607; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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OY 180 GACAACATGCTCGGGGGGACAGAAATTTGGCGCTTACGCAAGGCTTTCATGACCAAGG 239
Db 189 GACAACATGCTCGGGGGGACAGAAATTTGGCGCTTACGCAAGGCTTTCATGACCAAGG 248
OY 240 AAATCATATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 299
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OY 420 CGCCTTACTGCTGCTGATTCATCCCGCCAGTGGCGGAGTCTAATTAATTAATCAAC 479
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RESULT 14
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DEFINITION BG687423 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4762436 5',
mRNA sequence.
ACCESSION BG687423
VERSION   BG687423.1 GI:13918820
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 711)
AUTHORS   NIH-MGC http://mgi.mcl.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L16C1616 row: h column: 21
High quality sequence stop: 704.

FEATURES
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/note="Organ: Lung; Vector: pMDR-LIB (Clontech); Site_1:
SfiI (ggcgccctcgccg); Site_2: SfiI (ggcgctatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAAGGCCAGGCGGCGGACATG-dT(30)-BN-3'-
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
Library."
BASE COUNT 220 a 152 c 148 g 191 t
ORIGIN

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GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
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Title: US-10-006-190-2

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Sequence: 1 GCCAGCCCAAGCCCTGCT.....TCGAATATATATTACTTTTA 854

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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/pcodata/1/lna/6B.COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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16	35.2	4.1	28882	4	US-08-961-527-140
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22	33.8	4.0	388	4	US-09-378-074-1
23	33.8	4.0	388	5	PCT-US93-07370-1
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25	33.8	4.0	1367	3	US-08-475-742-3
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29	33.8	4.0	1370	4	US-09-060-694-17	Sequence 17, Appl
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31	33.8	4.0	1370	5	PCT-US93-07370-17	Sequence 3, Appl
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33	33.8	4.0	1466	1	US-07-928-611-19	Sequence 19, Appl
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37	33.8	4.0	1466	5	PCT-US93-07370-19	Sequence 5, Appl
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44	33.8	4.0	4524	2	US-08-845-998-7	Sequence 7, Appl
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## ALIGNMENTS

RESULT 1  
US-08-829-027-2  
Sequence 2, Application US/08829027  
Patent No. 5856160  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/829,027  
FILING DATE: Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0256 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 854 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Consensus  
CLONE: 2122022  
US-08-829-027-2  
Query Match 99.6%; Score 851; DB 2; Length 854;  
Best Local Similarity 100.0%; Pred. No. 2.3e+248;  
Matches 854; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
 US-09-225-366-2  
 Sequence 2, Application US/09225366  
 Patent No. 6001624

GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Shah, Purvi  
 TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/225.366  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/829,027  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0256 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 854 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: Consensus  
 CLONE: 2122022  
 US-09-225-366-2

Query Match 99.6%; Score 851; DB 3; Length 854;  
 Best Local Similarity 100.0%; Pred. No. 2,3e-248;  
 Matches 854; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 361 GAGCTTATCAGATCGACACAGTATGATTAACCTGATGATGATGATGATGATGATGATGATGAT 420  
 DB 361 GAGCTTATCAGATCGACACAGTATGATTAACCTGATGATGATGATGATGATGATGATGATGAT 420  
 QY 421 GCCTTACTGCTGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
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 QY 481 CTCGCCAAACCTGGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

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Db 661 TTGGCCCATATGATATGCTTTCTTCTACAACTAAAGTTCCACAAGACGAGAACTT 720
QY 721 CAGTACTCATGAGGAAATGTGTAACTATTAACTAGATGAGATGGCAAACTCTCTA 780
Db 721 CAGTACTCATGAGGAAATGTGTAACTATTAACTAGATGAGATGGCAAACTCTCTA 780
QY 781 GTCCCTTCATTTAGAACCTGCTTTTCTTCTAGACTTCTAGATGATGAAATCTTGAAA 840
Db 781 GTCCCTTCATTTAGAACCTGCTTTTCTTCTAGACTTCTAGATGATGAAATCTTGAAA 840
QY 841 TTATATTACTTTTA 854
Db 841 TTATATTACTTTTA 854
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RESULT 3
US-09-149-476-68
; Sequence 68, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
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; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,888	EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,894	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636	EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,864	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,599	EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588	EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585	EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586	EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590	EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594	EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589	EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593	EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614	EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501	EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964	EARLIER APPLICATION NUMBER: 60/048,964

- EARLIER FILING DATE: 1997-06-06  
 - EARLIER APPLICATION NUMBER: 60/057,650  
 - EARLIER FILING DATE: 1997-09-05  
 - EARLIER APPLICATION NUMBER: 60/056,884  
 - EARLIER FILING DATE: 1997-08-22  
 - EARLIER APPLICATION NUMBER: 60/057,669  
 - EARLIER FILING DATE: 1997-09-05  
 - EARLIER APPLICATION NUMBER: 60/049,610  
 - EARLIER FILING DATE: 1997-06-13  
 - EARLIER APPLICATION NUMBER: 60/061,060  
 - EARLIER FILING DATE: 1997-10-02

Query Match	97.8%;	Score 835.2;	DB 4;	Length 1751;
Best Local Similarity	99.2%;	Pred. No. 2.1e-243;		
Matches 848; Conservative	0;	Mismatches 6;	Indels 1;	Gaps 1;

QY	1	GGCAGCCCAAGAACCTGGTACCCGCGGGTG-6GGGCTCAGTCTCGGCAATGGGAGGG	59
Db	44	GGCAGGCCAAGACCTGGTACCCGCGGGTGCAGTCTCGGCAATGGGAGGG	10
QY	60	TCCGCGGGCTCTCGAGACGGTGATCATGGGGGGCCCCGGGCTCGGGCAAGGACCGTG	11
Db	104	TCCGGCGGGCTCTCGAGACGGTGATCATGGGGGGCCCCGGGCTCGGGCAAGGACCGTG	16
QY	120	TGCTGGCGATACATCAACACTGTGAGTGAAGACCTCCACGCGGGAGCTCGTCCGG	17
Db	164	TGCTGGCGATACATCAACACTGTGAGTGAAGACCTCCACGCGGGAGCTCGTCCGG	22
QY	180	GACACATCCTCGGGGGACAGAAATTTGGCTGTTCACCAAGGCTTTCATTGACCAAGG	23
Db	224	GACACATCCTCGGGGGACAGAAATTTGGGCTGTTCACCAAGGCTTTCATTGACCAAGG	28
QY	240	AAACTCATCCAGATGATGTATCATGACTCGGCTGGCCCTTATAGCTGAAAAATCTCAC	29
Db	284	AAACTCATCCAGATGATGTATCATGACTCGGCTGGCCCTTATAGCTGAAAAATCTCAC	34
QY	300	CAGTATAGCTGGCTGTGGATGGTTTTCAAAGGACATTCACAGGACAGAGCCCTAGAT	35
Db	344	CAGTATAGCTGGCTGTGGATGGTTTTCAAAGGACATTCACAGGACAGAGCCCTAGAT	40
QY	360	AGAGCTTATCAGATCGACACAGTGAATTAACCTGAATGTGCCCTTGGAGTCAATTAACA	41
Db	404	AGAGCTTATCAGATCGACACAGTGAATTAACCTGAATGTGCCCTTGGAGTCAATTAACA	46
QY	420	CGCTTACGTCGCTGGATTCATCCGCGACGTGGCCGATCATATTAACCTTAATTTCAAC	47
Db	464	CGCTTACGTCGCTGGATTCATCCGCGACGTGGCCGATCATATTAACCTTAATTTCAAC	52
QY	480	CCGCCCAAAACGTGGGATGTGATGACCTGACTGGGAGGCTCTTCATTAAGCTGAGAT	53
Db	524	CCGCCCAAAACGTGGGATGTGATGACCTGACTGGGAGGCTCTTCATTAAGCTGAGAT	58
QY	540	GATTAACCGAGACGGTATCAAGACATAAGGCTTATGAGACCAACAAAGCAACGACG	59
Db	584	GATTAACCGAGACGGTATCAAGACATAAGGCTTATGAGACCAACAAAGCAACGACG	64
QY	600	CTGGNATTTTACCAAAAAAGGGGTGTGAAACATTTCCGGACACAAACCAACAG	65
Db	644	CTGGNATTTTACCAAAAAAGGGGTGTGAAACATTTCCGGACACAAACCAACAG	70
QY	660	ATTGGCCCTATGTATGTCTTCTCTCAACATAAAGTTCCACAAAGAACCCAGAAAGCT	71
Db	704	ATTGGCCCTATGTATGTCTTCTCTCAACATAAAGTTCCACAAAGAACCCAGAAAGCT	76
QY	720	TGAGTTACTCCATGAGGAGAAATGTGTGTAATTTATATAGTAAGATGGGCAAACTCTCT	77
Db	764	TGAGTTACTCCATGAGGAGAAATGTGTGTAATTTATATAGTAAGATGGGCAAACTCTCT	82
QY	780	AGACCTTGATTTAAACCTCTTTCTCTTAAGACTTCAGATATGATGTAATTTCTTTGAA	83
Db	824	AGACCTTGATTTAAACCTCTTTCTCTTAAGACTTCAGATATGATGTAATTTCTTTGAA	88
QY	840	ATTATATTAATTTTA 854	



Db 11402 CAC-----AGTGAATTAAGAGAGATTAATCAACAGCTGAAGATG 11446  
QY 541 ATAACAGAGAGCTTATCAAGACTAAGCTTATGAAGCCAAACAAAGNCAGTCC 600  
Db 11447 ATAGAGCTGAGAGAGAAAGCTGTTGAGATTAATTTGCTCAAGAGAAACATCA 11506  
QY 601 TGGNATATTACAGAAAGAGGGGCTGGAACATTCCTCCGAGACAGAAACCAAGA 660  
Db 11507 TTGCTCAGTACCGTGGCAAGAGTTGGTTCATGACATCCAGAGTAATCAAGATATCAAG 11566  
QY 661 TTGGCCCTATGATATGCTTTCTCAAACTAAAGTCCACAAAG 706  
Db 11567 ATGCTCTTCAGATATTGAAAAAGTATGCAAAATTTGAATTAAG 11612

RESULT 6  
US-08-125-468-1/c

; Sequence 1, Application US/08125468  
; Patent No. 5589385  
; GENERAL INFORMATION:  
; APPLICANT: Ryan, Michael J.  
; APPLICANT: Lotvin, Jason A.  
; APPLICANT: Strathy, Nancy  
; APPLICANT: Fantini, Susan E.  
; TITLE OF INVENTION: Cloning of the biosynthetic pathway for  
; TITLE OF INVENTION: chlorotetracycline and tetracycline formation and cosmid  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07470  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/125,468  
; FILING DATE: 22-SEP-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Tsevdos, Estelle J  
; REGISTRATION NUMBER: 31,145  
; REFERENCE/DOCKET NUMBER: 31,255-02  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (201)831-3241  
; TELEFAX: (201)831-3305  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30001 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-125-468-1

Query Match 4.7%; Score 40; DB 1; Length 30001;  
Best Local Similarity 50.0%; Pred. No. 0.15;  
Matches 100; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 76 GAGCGGTGATCATGGGGGCGGCTCGGCAAGGACCGCTGTCGCGCATCACTA 135  
Db 5393 GGGCGGTGCTGCTGGCTCCACCGCGCCGCTGCTGCGCGCACCGCGC 5534  
QY 136 CACACTTGAGCTGAAGCACTCTCCAGGGGAGGACCTGCTCGGAGCAACATGCTCGGG 195  
Db 5533 TGGCCCGGCGCTGCTGACCGGTGGGCGCGCTGCGCGGATCAACGCGCGGCGC 5474

QY 196 GCACAGAAATGGCGTGTAGCCAGGCTTTCATTTGACCAAGGAGAAATCATCCAGATG 255  
Db 5473 GCAGAGTCAGAGGCGCGGATGATCGGGGCTTTCGGGAGACTGGCCCTGACCGGACA 5414  
QY 256 ATGTCATGACTGGGTGGCC 275  
Db 5413 GCCCGCTCACCGCGCGGCC 5394

RESULT 7  
US-08-474-933-1/c

; Sequence 1, Application US/08474933  
; Patent No. 5866410  
; GENERAL INFORMATION:  
; APPLICANT: Ryan, Michael J.  
; APPLICANT: Lotvin, Jason A.  
; APPLICANT: Strathy, Nancy  
; APPLICANT: Fantini, Susan E.  
; TITLE OF INVENTION: Cloning of the biosynthetic pathway for  
; TITLE OF INVENTION: chlorotetracycline and tetracycline formation and cosmid  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07470  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,933  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/125,468  
; FILING DATE: 22-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Tsevdos, Estelle J  
; REGISTRATION NUMBER: 31,145  
; REFERENCE/DOCKET NUMBER: 31,255-02  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (201)831-3241  
; TELEFAX: (201)831-3305  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30001 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-474-933-1

Query Match 4.7%; Score 40; DB 2; Length 30001;  
Best Local Similarity 50.0%; Pred. No. 0.15;  
Matches 100; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 76 GAGCGGTGATCATGGGGGCGGCTCGGCAAGGACCGCTGTCGCGCATCACTA 135  
Db 5593 GGGCGGTGCTGCTGGCTCCACCGCGCCGCTGCTGCGCGCACCGCGC 5534  
QY 136 CACACTTGAGCTGAAGCACTCTCCAGGGGAGGACCTGCTCGGAGCAACATGCTCGGG 195  
Db 5533 TGGCCCGGCGCTGCTGACCGGTGGGCGCGCGCTGCGCGGATCAACGCGCGGCGC 5474  
QY 196 GCACAGAAATGGCGTGTAGCCAGGCTTTCATTTGACCAAGGAGAAATCATCCAGATG 255  
Db 5473 GCAGAGTCAGAGGCGCGGATGATCGGGGCTTTCGCGGACTGCGCCCTGCGGCTACCGGACA 5414

QY 256 ATGTCATGACTGGCTGGCC 275  
DB 5413 GCCCGCTCACCGCCGCC 5394

## RESULT 8

US-08-822-586-45  
; Sequence 45, Application US/08822586  
; Patent No. 6015890

## GENERAL INFORMATION:

APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND  
APPLICANT: AMALIO TELENTE  
TITLE OF INVENTION: AN EMBCAB OPERON OF MYCOBACTERIA AND  
TITLE OF INVENTION: MUTANTS THEREOF  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN  
STREET: 90 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: U.S.A.  
ZIP: 10016

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE  
MEDIUM TYPE: DISKETTE  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/822,586  
FILING DATE: MARCH 20, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: ELIZABETH A. BOGOSIAN  
REGISTRATION NUMBER: 39,911  
REFERENCE/DOCKET NUMBER: 96700/437  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 697-5995  
TELEFAX: (212) 286-0854 or 286-0082  
TELEX: TWX 710-581-4766

## INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10095  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
US-08-822-586-45

Query Match 4.5%; Score 38.8; DB 3; Length 10095;  
Best Local Similarity 51.1%; Pred. No. 0.19; Mismatches 87; Indels 0; Gaps 0;

Matches 91; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 13 GCCCTGTGACCCGCGGCTGCGGCTCAGTCTGCGGCCATGGGGCGCTCCGCGGCTGC 72  
DB 4854 GCGGGGCGCATGTGACTGTGCGCCGCGTGGCGGTGCGCGCGGCGGCTTTCCTGA 4913  
QY 73 TCGGACGGTGATCATGGGGGCGCGGCTCGGGCAAGGGCAGCGTGTGTCGCGCATCA 132  
DB 4914 TCACCTGTGTGGTTCGGGACACAGCCGTGCGCACGGTGGCGCATCGGCGCATCA 4973  
QY 133 CTACACACTTGCAGTGAAGCACTCTCCAGCGGGAGCCGTGTCGGGACAAATGCT 190  
DB 4974 AGTACAAGTGGCGCCGACCATGCTGTGTACCAAGACTTCTGCGCTACTACTTCT 5031

## RESULT 9

US-09-221-017B-913  
; Sequence 913, Application US/09221017B  
; Patent No. 6444789

## GENERAL INFORMATION:

APPLICANT: ROSS, Bruce C.  
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF

NUMBER OF SEQUENCES: 1120

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FORSTER

STREET: 755 PAGE MILL ROAD

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/221,017B

FILING DATE: 23-DEC-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP1182

FILING DATE: 31-DEC-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP1546

FILING DATE: 30-JAN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP2911

FILING DATE: 09-APR-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU98/01023

FILING DATE: 10-DEC-1998

ATTORNEY/AGENT INFORMATION:

NAME: Monroy, Gladys H

REGISTRATION NUMBER: 32,430

REFERENCE/DOCKET NUMBER: 27340-20021.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-813-5600

TELEFAX: 650-494-0792

INFORMATION FOR SEQ ID NO: 913:

SEQUENCE CHARACTERISTICS:

LENGTH: 4530 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: UNKNOWN

ORIGINAL SOURCE:

ORGANISM: PORPHYROMONAS GINGIVALIS

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1...4530

US-09-221-017B-913

Query Match 4.5%; Score 38.4; DB 4; Length 4530;  
Best Local Similarity 48.0%; Pred. No. 0.16;

Matches 142; Conservative 0; Mismatches 151; Indels 3; Gaps 1;

QY 68 GCTGCTGCGAGCGGTGATCATGGGGGCGCGGCTGCGGCAAGGCACCTGTGTCGG 127  
DB 4131 GATGCTTAACGTAATATCTTCGCTCCGCTCCGGGGAAGGCGCCAAAGCGAAGA 4190  
QY 128 CATCACTACACACTTGAGCTGAAGCACTCTCAGCGGGGAGCTGCTCGGGCAACAT 187  
DB 4191 ACTGATTCCTGATGATGATTCGCGCATATTTCAACCGGAGATGTGCTTGTGCCAAT 4250  
QY 188 GCTCGGGGCGCAAAATGGCGTGTAGCCAAAGCTTTCATTGACCAAGGAATCAT 247  
DB 4251 CAAAGCTCAGACCGAAGTGGGCAAGAGCGCGGCTATCATCAAGAGGACACCTCGT 4310  
QY 248 CCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 304  
DB 4311 ACCTGACAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4370









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